

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 99145

TO: Sheridan Swope

Location: cm1/12D12/10D01

Art Unit: 1652

Friday, July 18, 2003

Case Serial Number: 09/966880

From: Barb O'Bryen

Location: Biotech-Chem Library

CM1-6A05

Phone: 308-4291

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barbara.obryen@uspto.gov

Search Notes	



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AL559877 LTL_FL011_BC1 Homo sapiens cDNA clone CSODG003YB14 5 prime
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                                                                                                                         481 ACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTC 540
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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/sex="male"
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/db_xref="taxon:9606"
/clone="IMAGE:95997"
/clone=lib="NMH-MGC-99"
/tissue_type="lymphona, cell line"
/lab.host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: p07B7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming, Directionally cloned
into EcoRI/XhoI sites using the following 5 adaptor:
GGCAGGG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2108 row: p column: 10
High quality sequence stop: 634.
Location/Ounlifiers
Location/Ounlifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Organ: B-cells; Vector: poTB7; Site_1: Xho1; Site="Organ: B-cells; Vector: poTB7; Site_1: Xho1; Site_2: ECCRI; cDNA made by Oligo-dT priming.

Directionally cloned into ECCRIXANOI Sites using the following S' adaptor: GCCACGAG(G). Size-selected >500bp for average insert size 1 8 Rb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis klt (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MCC Library."
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/lab_host."DH10B (phage-resistant)"
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                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_48"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 872)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
CATGAAAGAACTTTCAAAGCCTGGGAAGGCTGCATGAAAATTCAGTTCGTCTCTCCCAGA
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Gapbbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                 TGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTG
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1052 bp mRNA linear EST 29-MAR-2002 AGENCOURT_6796291 NIH_MGC_99 Homo sapiens cDNA clone IMACE:5808181 BQ055935
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1052)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Rlabte: LLCM2051 row: m column: 14
High quality sequence stop: 665.
GCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTG
                 242 CCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTG
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone=lib="IMAGE:4766234"
/clone=lib="MHLMGC_48"
/clone=lib="MHLMGC_48"
/lissue_type="primary B-cells from tonsils (cell line)"
/lab_bost="DHLOB (phage-resistant)"
/note="Organ: B-cells; Vector: porB7; Site_1: XhOI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: gGAACGAGG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Plate: LLCM1656 row: g column: 03
High quality sequence stop: 740.
Location/Qualifiers
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ive 0; Mismatches
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/note="Organ: lymph, vector: pOTB7; Site_l: XhoI; Site_2:
ECORI; CDNA made by oligo dT priming. Directionally cloned
into EcoRIX/KhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of Califorinia, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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BG754140 664 bp mRNA linear EST 15-MAY-2001 602709681F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846005 5', mRNA sequence.

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                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Tissue Procurement: Louis M. Standt, M.D., Ph.D.

Tissue Procurement: Louis M. Standt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCMIGG row: b column: 22

High quality sequence stop: 662.
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                                                                                                                                                                                                                                                                                                  National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Mismatches
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                                                                                                                                                                                                 Mammalia; Eutheria; Primates;
1 (bases 1 to 664)
                                                                                                                                                            Eukaryota; Metazoa; Chordata;
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tive 0;
GI:14064793
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665 TTGGGACTTTGATAGCAACTTCCAGGAATGTCACCACGATGAAATATCTCTGCTGAAGA 724 11111111111111111111111111111111111		332 GITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1145 TCTTCCATCAGGCCATGATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGTGACC 1204	SULT 8 SULT 8 SULT 8 SULT 8 BG757089 B20 bp mRNA linear EST 15-MAY-2001 FINITION 602715124F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855517 5', CESSION BG757089.1 GI:14067742 WWORDS EST. ORCE human BURNALSA HOMO sapiens EUKARYOCA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0	0 O O O O O O O O O O O O O O O O O O O	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 8 BG757089 LOCUS DEFINITION ACCESION VERSION KEYWORDS SOURCE ORGANISM	AUTHORS TITLE JOURNAL COMMENT FEATURES
Oy 1054 TTATTATTGATTGAGTTAACAGTGGTGTTAGTGATAGATTTTCTATTCTTT 1113	Qy 1234 CAATCATGTTTTAATCAGCAGAAGCATGTTTTATGTACAAAGAAG 1293 Db 602 CAATCATGTTTTAATCAGCAGAAGCATGTTTTTATGTTTGTACAAAGAAG 661 Qy 1294 ATT 1296 11 Db 662 ATT 664	RESULT 7 B075526 LOCUS B075526 LOCUS B075526 LOCUS DEFINITION 602716206F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856568 5', ACCESSION B075526 VERSION B075526.1 GI:14066179 KEYWORDS EST. OUR CE PURE ACCESSION CONTROL OF THE ACCESSION CONTROL OF		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.lln.gov http://image.lln.gov Plate: LiCM1707 row: k column: 01 High quality sequence stop: 638. Location/Qualifiers source /organism="Homo sapiens" /dlone="In-MAC.48" /clone="In-MAC.48" /tlssue_type="Primary B-cells from tonsils (cell line)" /tab_host="BH108 (phage-resistant)" /tab_host="BH108 (phage-resistant)" /note="Organism-BH008 (phage-resistant)" /note="Organism-BH008 (phage-resistant)"	Site_2: ECORI; CDNA made by oligo-dr priming. Directionally cloned into ECORI/Xhor sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagane) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." Note: this is a NIH_MGC Library." Ouery Match Query Match 21.6%; Score 608; DB 12; Length 820; Best Local Similarity 100.0%; Pred. No. 0; Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

pe

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/issue_type="primary" B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: porB7; Site_1: XhoI;
Site_2: EcorI: cond made by oligo-dT priming.
Directionally cloned into EcoRIXXhoI sites using the following 5' adaptor: GGAKGAGG(G). Size-selected >SObp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                   Enteleostomi;
                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLCM1209 row: n column: 19
High quality sequence stop: 692.
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                                                                                                                   1 (bases 1 to 693)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                   Catarrhini; Hominidae;
                                                                                 Chordata; Craniata; Vertebrata;
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/db_xrefa"taxon:9606"
/clone="IMAGE:4336722"
/clone_lib="NIH_MGC_48"
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8
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               GI:12342311
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Mammalia; Eutheria;
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                                                                               /issue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage_resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI: conA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGAGGAG(G). Size-selected >500bp for a verage insert size I.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Pred. No. 0;
0; Mismatches
                       /organism="Homo sapiens"
                                                                     /clone_lib="NIH_MGC_48"
                                   /db_xref="taxon:9606"
/clone="IMAGE:4855517"
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ilarity 99.8%;
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724 ALGORDARAMARGEDENTICATECTOTITITATICTTCATACTCCCTT[480 785 7745047 785	/db_xref= /clone="] /clone="] /lab_host /note=="] /note=="] Site_2: b Direction for averre		/ative 0; Mismatcl 	Match Qy Db Qy Db
724 ACAGTGGATAMANANGNGTCCTTCAGTTTTTATTCTTCACTTT 783 725	urce	FEATUI	19.8%; Score 558; DB 12; Length 670; Similarity 100.0%; Pred. No. 0; 8; Conservative 0; Mismetches 0; Indels 0; Gaps	Query Best Match
724 ACAGGGGAAAAAACAGCCCTCCAAGCCTCCTGGTTTTTATCTCCAACTCCACTTT 783 421 [BASE CO
11		REFER AUTI TITI JOU COMMEI	/organism="Homo sapiens" /db_xref="twon:9606" /clone='IMAGE:457648" /clone_lib="NIH_MGC_48" /tissue_type="primary B-cells from tonsils (cell line)" /tab_host="MulDB (phage-resistent)" /note="Organ: B-cells; Vector: pOTB7; Site_1: xhoI; Site_2: EcoRI: cDNA made by oligo-dT priming.	
724 ACAGTGGATAAAAACAGTCCTTCAAGTCTTCTCTTTTTTTT	BF238155.1 BF238155.1 EST. human.	ACCESS VERSIC KEYWOI SOURCI	http:/ Plate: High c	FEATURE
724 ACAGTGGATAAAAACAGTCCTTCAAGTCTTCTTCTTCTAACTCTTCAACTCTTT 783 421 ACAGTGGATAAAAACAGTCCTTCAAGTCTTCTTCTTCTAACTCTTCAACTTTT 783 422 ACAGTGGATAAAAAAAAAAAAAAAAAAAAAAAAATTTTATTTTTT	7	RESUL BF238 LOCUS DEFIN	Ω	
724 ACAGTGGATAAAAAACAGTCCTTCAAGTCTTCTAAACTCTCCAACTTT 783 [11111111111111111111111111111111111	1205 CCAAACCATCTCTCC	Qy		TITLE JOURN COMMENT
724 ACAGTGGATAAAAAACAGTCCTTCTAGTTTTTATTCTTCAACTCTTT 783 [11111111111111111111111111111111111		Qy Db		REFEREN
724 ACAGTGGATAAAAAACAGTCCTTCTAGTTTTTATTCTTCAACTCTTT 783 [11111111111111111111111111111111111		Qy		VERSION KEYWORD SOURCE ORGAN
724 ACAGTGGATAAAAAACAGTCCTTCTAGTTTTTATTCTTCAACTCTCACTTT 783		Qy	BG341546 670 bp mRNA linear EST 27-FEB 602463652F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576548 5 mRNA sequence.	LOCUS
724 ACAGTGGATAAAAAACAGTCCTTCTGTTTTTATTCTTCAACTCTCACTTT 783		λδ Q Δ		RESULT BG34154
724 ACAGTGGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		ąg qg	ATAGAGAAGGAACACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCAGTTT 89	Oy Db
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ganism="Homo sapiens"

xref="taxon:9606"

one="IMAGE:4054915"

one_lib="NHH_MGC-48"

one_lib="NHH_MGC-48"

one_lib="Unit primary B-cells from tonsils (cell line)"

b_host="DH10B (phage-resistant)"

te="Organ: B-cells; Vector: pOTB7; Site_1: Xhol;

e=_1 EcoRI; cDNA made by oligo-dT priming,

ectionally cloned into EcoRI/Xhol sites using the

lowing 5' adaptor: GGCAGGAG(G). Size-selected >500bp

average insert size 1.8kb. Library constructed by Ling
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                       AGGTCTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGCAA 904
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ia; Primates; Catarrhini; Hominidae; Homo.
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nnt: Louis M. Staudt, M.D., Ph.D.
reparation: Ling Hong/Rubin Laboratory
reparation: Ling Hong/Rubin Laboratory
by: Incyte Genomics, Inc.
Lion: MGC clone distribution information can be
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tes of Health, Mammalian Gene Collection (MGC)
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Strausberg, Ph.D.
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IMAGE:3080216 5', mRNA sequence.
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11H-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
     οĘ
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Email: cgapbs-remail.nih.gov
Eno II site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                              AATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCA
                                                                                                                                                                                                GAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGAGGAGGAGAAGA
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                                                                                                                  Length
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                                                                                                                    DB 12;
                                                                                                                  Query Match 19.2%; Score 540; DE Best Local Similarity 100.0%; Pred. No. 0; Matches 540; Conservative 0; Mismatches
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AW504807.1 GI:7142474
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (_LT1)"
/note="vector: pT773-Pac; Site_1: Not1; Site_2: Eco R1
Constructed from size fractionated cytoplasmic mRNA
(3.5.4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria d
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1351 AATAAAGGATCTTAAAATGGGCAGGAGGACTGTGAACAAGACACCCTAATAATGGGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 AATAAAGGATCTTAAAATGGGCAGGACGACTGTGAACAAGACACCCTAATAATGGCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 TGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAAGTCCCTAATTTAGA
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0
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www-bio.11nl.gov/bbrp/image/image.html
Seg primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.6%; Sco. 100.0%; Pred. No. c, 0. Mismatches
                                                                                                                                    /clone="IMAGE:3080216"
/clone_lib="NIH_MGC_50"
/tissue_type="lymph"
                                                                                                                /db_xref~"taxon:9606"
                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           120 g
                                                                     1. .570
/organism⊷"Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:14068045
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BG757392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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us-09-966-880a-7.100olig.rst

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Anotes Torgan: B-cells; Vector: porB7; Site_1: XhoI; Site_2: ECCRI; cDNA made by Oligo-dT priming.
Directionally cloned into BernYXhoI sites using the following 5' adaptor: GGRAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling then in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2.8P-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG686876 889 bp mRNA linear EST 01-MAY-2001
602650861F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763247 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GGAGGCAAGAAGACACTCTGGACACCACTATGGACAGCCTCTTGATGAACCGGAGGAGT 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgg.nci.nih.gov/.

NIH-MGC http://mgg.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCIMfol8 row: j column: 16

High quality sequence stop: 727.

High quality sequence stop: 727.
482 TGCAAATAGCCATCATGACCTTCAAAGATTATCTTTACTGCTGGAATACTTTTGTAGAAA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="primary B-cells from tonsils (cell line)" /lab_host="DH10B (phage-resistant)"
                                                   GACAGCTTCGGCCCATCCTTTTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 GGAGGCAAGAAGACACTCTGGACACCACTATGGACAGCCTCTTGATGAACAACAGGAAGAAGT
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Pred. No. 0;
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/clone_lib="NIH_MGC_48"
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BG686876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGAGAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGAGGCAAGA 60
                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM1694 row: k column: 05
High quality sequence stop: 693.
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                    NIH, MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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1 (bases 1 to 604)

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Hol., I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element CDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                           ACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTG
                                                                                                                                                                                                                                              ACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCA
                                                                           ATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAG
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, hote="Vector: plluescriptSKm"
121 c 109 g 184 t
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Plate: 394
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Matches 44
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ACCESSION
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BF975166 942 bp mRNA linear EST 22-JAN-2001
602244657F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335639 5',
                                                                                GGACTGTGAACAAGACACCCTAATAGGTTGATGTCTGAAGTAGCAAATCTTCTGGAA 1436
                                                                                                                                                                  ACGCAAACTCTTTTAAGGAAGTCCCTAATTTAGAAACACCCACAAACTTCACATATCATA 1496
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I (bases 1 to 942)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M Staudt, M.D., Ph.D.

CONDA Library Preparation: Ling Homy/Rubin Laboratory

CDNA Library Preparation: Ling Homy/Rubin Laboratory

CDNA Library Preparation: Ling Homy/Rubin Laboratory

CDNA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL)

Plate: LicM1207 row: a column: 16
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TATAGACCATGCATGGTCACCTTCAAGCTACTTTAATAAAGGATCTTAAAATGGGCAGGA
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High quality sequence stop: 707.
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/db_xref="taxon:9606"
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a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NHL19W, testis NHT, and B-cell NOT_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento soarses and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               602323871F1 NIH_MGC_89 Homo sapiens CDNA clone IMAGE:4426960 5', mRNA sequence.
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1 (bases 1 to 511)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Issue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                        Score 442; DB 9; Length 442;
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                                                                                                                                                                                                                                                                                                                                                                              542 CATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGA 601
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1 (bases 1 to 442)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 426 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 433.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCTGGCCGC
                                                                                                                                                                                                                                                                                       TGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCCGACATGTG
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   Length 942;
                                        Indels
                                        1;
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     DB 12;
                                        0; Mismatches
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/db_xref="taxon:9606"
       Score 448;
                        Pred. No.
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Euteleostomi;

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Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB31307 353 bp mRNA linear EST 20-FEB-1998 oc70a06.s1 NCL_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1355026 3' similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1144 CTCTTCCATCAGGCCATGATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGTGAC 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1204 CCCAAACCATCTCTCCAAAGCATTAATATCCAATCATGCGCTGTATGTTTTAATCAGCAG 1263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Enail: cgapbs-remail.nih.gov
Eno RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bic.llni.gov/bbrp/image.html
Seq primer: MI3 Forward
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                            1 (bases 1 to 374)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="germinal center
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
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/tissue_type="lymph"
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/clone="IMAGE:3054318"
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                                                                                                                                                                                        /organism="nowcorrections" / organism="nowcorrections" | / organism="nowcorrections" | / organ="lib="Nih-MGC_89" | / clone="lib="Nih-MGC_89" | / tissue_type="hypernephrome, cell line" | / tissue_type="hypernephrome, cell line" | / lib=host="hypernephrome, cell line" | lib=host="hyper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 511;
                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10174 row: n column: 17
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%; Score 380; DE
99.8%; Pred. No. 0;
tive 0; Mismatches
                                                                                                 High quality sequence stop: 511.
Location/Qualifiers
1. 511
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Gaps

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65

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AML3534/
476 bp mRNA linear EST 29-OCT-1999 UI-H-BII-acg-e-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714208 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-rémail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 476).
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
53 GCGAACCGTGCACACGCTCATAGTTCTAGCTGCTTGGGAGGTTGAGGAGGGA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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TAG_TISSUE=lung
TAG_SEQ=CAAC"
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                                                                                                                                                                                          AW135547.1 GI:6139680
                                                                                                                                                                                                                                                   Homo sapiens
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KEYWORDS
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                                                                            RESULT 21
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                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ph.D., Gerald Marti, Mod. Bento Soares, Ph.D., David Aliman, Contained Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. Debarty Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image.html
Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1385 AACAAGACACCCTAATAATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAAC 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1445 TCTTTTAAGGAAGTCCCTAATTTAGAAACACCCACAAACTTCACATATCATAATTAGCAA 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1505 ACAATTGGAAGGAAGTTGCTTGAATGTTGGGGAGAGGAAAATCTATTGGCTCTCGTGGGT 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1565 CTCTTCATCTCAGAAATGCCAATCAGGTCAAGGTTTGCTACATTTTGTATGTGTGATG 1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1625 CTTCTCCCAAAGGTATATTAACTATATAAGAGTTGTGACAAAACAGAATGATAAAGCT 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. (Lase, 1 to 353)
NCI-GAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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AA831307.1 GI:2904406
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                                                      Homo sapiens
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1361 CTTAAAATGGGCAGGAGGACTGTGAACAAGACACCCTAATAATGGGTTGATGTCTGAAGT 1420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI468242 30-MAR-1999
tg35g05.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2110808 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 GCTACATTTTGTATGTGTGTGTGTGTGTTCTCCCAAAGGTATATTAACTATATAAGAGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1421 AGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAAGTCCCTAATTTAGAAACACCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Two Approaches To Facilitate Gene Discovery. Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.3%; Score 346;
100.0%; Pred. No.
Live 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Research 6, 791-806.
TAG_LIB~NCI_CGAP_Lym2
TAG_TISSUE~lymph node
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_SEQ=AAATG'
111 c
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AI468242.1 GI:4330332
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Matches 346;
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AW452648
BM452648.1 GI:6993424
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
The sequence contained an oligo-dT track that was present in the oligoucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                            1072 TGAGTTAACAGTGGTGTTAGTGATAGATTTTCTATTCTTTTCCCTTGACGTTTACTTTC 1131
                                                                                         ö
                                                                                                                                                                                                                                                  CTAAAGTGTCAACGTTTTTCTATGACTTTTAGGTAGGATGAGAGCAGAAGGTAGATCCTA 1011
                                                                                                                                                                                                                                                                                                              1012 AAAAGCATGGTGAGAGGATCAAATGTTTTATATCAACATCCTTTATTATTTGATTCATT 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                          1132 AAGTAACACAAACTCTTCCATCAGGCCATGATCTATAGGACCTCCTAATGAGAGTATCTG 1191
                                                                                                                                                                                                                                                                                                                                              237
                                                                                                                                                                                                    416 GTTTTGAATGCAACATTGTCCCCTACTGGGAATAACAGAACTGCAGGACCTGGGAGCATC 357
                                                                                                                                                                                                                                                                                                                                                                                                        176 AAGTAACACAAACTCTTCCATCAGGCCATGATCTATAGGACCTCCTAATGAGGAGTATCTG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 46). NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 4-123, >ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:3068708"
/clone_lib="NOT_CGAP_Subs"
/lab_host==1HU08 (Life Technologies)"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
                                                                                                                                                       476 TATGTCTTGAAAATAGAGAAGGAACACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCA
                                                                                                                                                                                                                                                                     TATGTCTTGAAAATAGAGAAGGAACACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCA
                                                                                                                                                                                       GTTTTGAATGCAACATTGTCCCCTACTGGGAATAACAGAACTGCAGGACCTGGGAGCATC
                                                                                         ;
0
                                                          Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GETGATTGTGACCCCAAACCATCTCTCCAAAGCATTAATA 77
                                                          DB 10;
             μ
                                                                                         0; Mismatches
             143
                                                        Score 349; 1
Pred. No. 0;
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/db_xref="taxon:9606"
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             98
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                                                          12.4%;
99.8%;
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Unpublished (1997)
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                                                               Query Match
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AW452648/c
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                             ORIGIN
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1540

1600

EST 30-MAR-1999

1480

Gaps

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Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 01-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1342 AGCTACTTTAATAAAGGATCTTAAAATGGGCAGGAGGACTGTGAACAAGACACCCTAATA 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1402 ATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAAGTCCC 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTTGAATGTTGGGGAGAGAAATCTATTGGCTCTCGTGGGTCTCTTCATCATCAGAAAT 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 ATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAAGTCCC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dr. Average insert size 1.25 kb. Life Technologies
catalog #: 11847-015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 GCTTGAATGTTGGGGAGAGGAAAATCTATTGGCTCCTCGTGGGTCTCTTCATCTCAGAAAT 342
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363 bp mRNA linear EST 01-DEC-199
Af79007.x1 Soares_fetal_liver_spleen_LNR5_5.1 Homo sapiens cDNA
clone IMAGE:1850892 3' similar to contains Alu repetitive element
;contains element L1 repetitive element ;, mRNA sequence.
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I ( bases 1 to 413) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="lymphoma, follicular mixed small and large
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:3002311"
/clone_lib="NGI_CGAP_Lym12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 411.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40UP from Gibco
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                     AW768364.1 GI:7700383
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Unpublished (1997)
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                                                                                       Homo sapiens
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    AW768364
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                                                                 human.
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                   1...321
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InAGE:110606"
/clone=lib="Soares_NFL_T_GBC_SI"
/lab_host="hullos"
/robe="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728111, and 729096-731399; Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hk73d04.xl NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3002311 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1608 TTTGTATGTGTGTGTGCTTCTCCCAAAGGTATTTAACTATAAGAGAGGTTGTGACAA 1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1728 TGAGGAGGAGGATGGCTTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACATAACAAGA 1787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 CATATCATAATTAGCAAACAATTGGAAGGAAGTTGCTTGAATGTTGGGGAAGAGGAAAATC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                    1 (bases 1 to 321)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This Consortium (info@image.llnl.gov) for further information.
Insert Length: 1095 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 TATTGGCTCTCGTGGGTCTCTTCATCTCAGAAATGCCAATCAGGTCAAAGTTTGCTACAT
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                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/note."Organ: B-cells; Vector: DOTB7; Site.1: Xho1; Site.2: ECORI; CDNA made by oligo-dT priming.

Site.2: ECORI; CDNA made by oligo-dT priming.

Site.2: Scori; CDNA made by oligo-dT priming.

Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologics).

Note: this is a NIH_MCC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATAGATTTTTCTATTCTTTTCCCTTGACGTTTACTTTCAAGTAACACAAACTCTTCCAT 1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1183 row: i column: 04
High quality sequence stop: 725.
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                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I thases I to 956)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host-"DH10B (phage-resistant)"
602146013F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309707 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 TGACTTTTAGGTAGGATGAGAGCAGAAGGTAGATCCTAAAAAGCATGGTGAGAGGATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTTTTTTATATCAACATCCTTTATTTTTTTCATT-TGAGTTAACAGTGGTGTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           794 ACAGAAAAATTTTATATACGACTCTTTAAAAAGATCTATGTCTTGAAAATAGAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 ACAGAAAAATATTTATATACGACTCTTTAAAAAGATCTATGTCTTGAAAATAGAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   854 AACACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGCAACATTGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 GATAGATTTTTCTATTCTTTTCCCTTGACGTTTACTTTCAAGTAACACAAAACTCTTCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organisme"Homo sapiens"
/db_xrefe"taxon:9606"
/clone="IMAGE:4309707"
/clone_libe"NJH_MGC_48"
                                                       BF664355.1 GI:11938351
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                     mRNA sequence.
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Best Local Similarity
Matches 417; Conserva
                                                                                                                 Homo sapiens
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                                                                                                human.
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                                                                             Euteleostomi;
                                                                                                                                                              Tunor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs:r@mail.inh.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1487 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 360.
                                                                                                             1 (bases 1 to 363)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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     GI:3844531
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EST 07-JUL-1998

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Euteleostomi;

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Anote—"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Site_1: NOt I: Site_2: ECO RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NDHI19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made IT. Thom the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239,
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nh.gov
This clone is available royalty-free through LLNL; contact the IMAGE Conscitum (info@imaga.lnh.gov) for further information.
Insert Length: 643 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
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IMAGE:1577758 3′, mRNA sequence.
AA954956
  GTATCTGGGTGATTGTGACCCCAAACCATCTCTCCAAAGCATTAATA 1231
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                   linear
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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101 c 100 q 150 t
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Pred. No. 0;
0; Mismatches
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/db_xref="taxon:9606"
                                                                                                                                             528 bp
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 422)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                      579
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -4UOP from Gibco
High quality sequence stop: 419.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2700581"
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                                                                                    RESULT 27
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   GGTTTGCTACATTTTGTATGTGTGTGATGCTTCTCCCAAAGGTATATTAACTATAAGA 1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. o column: 07
High quality sequence stop: 650.
                                                                                                                                                                                                                                                                                                                                   GAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACACGCTCATAGTTCTAGC
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                                                                                                                                                                                        152 GAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACACGCTCATAGTTCTAGC
                                                                     212 GGTTTGCTACATTTTGTATGTGTGTGTGCTTCTCCCCAAAGGTATTTAACTATAAGA
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1 (Dases 1 to 928)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 0;
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/db_xref="taxon:9606"
/clone="IMAGE:4566366"
/clone_lib="NIH MGC_48"
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/db_xref="taxon:9600"
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/clone="10="NoT_CGP_GCB_GCB_"
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                                                                                                                                                                                                                                                                                                                               AA504653 332 bp mRNA linear EST 18-AUG-1997 aa63f11.s1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:825645 3' similar to contains Alu repetitive element;, mRNA sequence.
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information can be
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157 TACTITCAAGTAACACAAACTCTICCAICAGGCCAIGATCIAIAGGACCTCCTAAIGAGA 98
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 332)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd.ET from Amersham
High quality sequence stop: 294.
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Email: cgapbs-r@mail.nih.gov
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AA504653.1 GI:2240813
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Matches 331; Conservative
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derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP_INST.

NCI_CGAP_PC21, NCI_CGAP_PC81, NCI_CGAP_CO10, NCI_CGAP_CO16, NCI_CGAP_PC161, NCI_CGAP_LC11, NCI_CGAP_LC12, NCI_CGAP_LC13, NCI_CGAP_LC13, NCI_CGAP_LC13, NCI_CGAP_LC14, NCI_CGAP_LC13, NCI_CGAP_LC13, NCI_CGAP_LC14, NCI_CGAP_LC14, NCI_CGAP_LC13, NCI_CGAP_LC14, NCI_CGAP_LC13, NCI_CGAP_LC13, NCI_CGAP_LC14, NCI_CGAP_LC14, NCI_CGAP_LC13, NCI_CGAP_LC14, NCI_CG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 939)
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TAG_TISSUE=germ cell
TAG_SEQ=AAATC"
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/organism="Homo sapiens"
/do_xref="taxon:9606"
/do_xref="taxon:9606"
/clone="IMAGE:2712644"
/clone="IMAGE:2712644"
/clone="IMAGE:2712644"
/lab_host="DH10B (Life Technologies)"
/note="vector: pr773D-pac (Pharmacia) with a modified
polylinker; Site=1: Not I; Site_2: Eco RI; The
NCI_CGAP_Sub3 library is a subtracted library derived from
the NCI_CGAP_Sub1 library, which is a subtracted library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nlb.gov
The sequence contained an oligo-dT track that was present in the oligonucleoutide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.lln.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 1-21,
                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTTTCTATGACTTTTAGGTAGGATGAGGAGGAAGGTAGATCCTAAAAAGCATGGTGA 1024
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                    CATTGTCCCCTACTGGGAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGTCAAC
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// Ab_xref="taxon:9606"
// Clone="InAcE="4576188"
// Clone=Lib="NHH_MGC_48"
// Clone=Lib="NHH_MGC_48"
// Clone=Lib="NHH_MGC_48"
// Lab_nost="butle (phage-resistant)"
// Ab_host="butle (phage-resistant)"
// Anote="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/XhoI sites using the
following 5' adaptor: GGGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscribt II RT (Life Technologies).
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                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incorpte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1288 row: h column: 13
High quality sequence stop: 547.
Location/Qualifiers
:ce
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
                                                                Contact: Robert Strausberg, Ph.D.
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Matches 207; Conserv
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TITLE
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SOURCE
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  AUTHORS
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AW444889 213-c-08-0-UI.sl NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733327 3', mRNA sequence.
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Email: capabs-remail.nih.gov
The Sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1659 TTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACACGCTCATACTTCTAGCTGC 1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1719 TTGGGAGGTTGAGGAGGGAGGATGGCTTGAACACAGGGTGTTTCAAGGCCAGCCTGGGCAAC 1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 TTGCTACATTTTGTATGTGTGTGATGCTTCTCCCAAAGGTATATTAACTATATAAGAGAG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_typew.hypernephroma, cell line"
/tissue_typew.hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: kidney; vector: pcMv-SpORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oliqo-dT primed.
Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

a 94 c 118 g 124 t
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1599 TIGCTACATTITGTATGTGTGTGATGCTTCTCCCAAAGGTATATTAACTATAAAGAGAG
CDNA Library Preparation: Life Technologies, Inc. (CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 517;
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                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10174 row: n column: 16
High quality sequence stop: 517.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12;
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www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%; Scc. 100.0%; Pred. No. v. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4426959"
/clone_lib="NIH_MGC_89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1779 ATAACAAGATCCTGTCTCAAAA 1803
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Mammalia; Eutheria;
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Unpublished (1997)
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Sequencing Center information can be

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). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL581406 507 bp mRNA linear EST 16-FEB-2001 AL581406 LTL_FL011_BC1 Homo sapiens cDNA clone CSOBG003YB14 3 prime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                        1 (bases 1 to 463)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cent
Clone distribution: NCI-CGAP clone distribution information carl
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -40ml3 fxd. ET from Amersham
High quality sequence stop: 126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            850 AAGGAACACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGCAACATTG
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                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:826619"
/clone_lib="NCI_CGAP_GCB1"
                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , mRNA sequence.
AL581406
AL581406.1 GI:12948375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.4
Best Local Similarity 100.
Matches 180; Conservative
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                                  Homo sapiens
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                                                                                                                 1279 TTTGTACAAAAGAAGATTGTFATGGGTGGGGATGGAGGTATAGACCATGCATGGTCACCT 1338
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TAG_LIB=NI_CGAP_Lym2
TAG_TISSUE=1ymph node
TAG_SEQ-AAAPG.
1 37 C 50 q 61 t
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                                                          /db_xref="taxon:9606"
/clone="IMAGE:2733327"
/clone=lib=NCI_GAP_Sub5"
/lab_host="DH10B (Life Technologies)"
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                Location/Qualifiers
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AA521498
POLYA-Yes
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BF664352
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                                                                                                                                                                                                                                                                                                                                                                                                        /note="vector: pcMvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 8900 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fullength.invitrogen.com" 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1471
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 268)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 685 Expers: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1412 GTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAAGTCCCTAATTTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 GTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAAGTCCCTAATTTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                         Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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0
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                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="B cells from Burkitt lymphoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.4%; Score 153; DB 9; Length 507; Best Local Similarity 100.0%; Pred. No. 0; Matches 153; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1532 TGGGGAGAAAATCTATTGGCTCTCGTGGGT 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 TGGGGAGGAAAATCTATTGGCTCTCGTGGGT 214
                                                                                                                                                                                                                          Location/Qualifiers
1. 507
/organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="cSODG003YB14"
/clone_lib="LTI_FL011_BC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA879422
AA879422.1 GI:2988533
                                                                                                                                                                                                                                                                                                                                                    /sex="male"
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AA879422/C
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AUTHORS
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AUTHORS
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SOURCE
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Anote—"Organ pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Ero RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I:M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1140 bp mRNA linear EST 21-DEC-2000 mRNA sequence.

BF663150 The ST 21-DEC-2000 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL.)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM1183 row: c column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 TGAAATGGAGTCTCAAAGCTTCATAAATTTATAAAACTTTAGAAATGATTCTAATAACAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 ACTITATIGACAGCAAATIGCTGCTGCCTCACTTCAAFCAGTFAAATAAATGATAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                /clone_lib~"Soares_NFL_T_GBC_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                  /organismu"Homo sapiens"/db_xrefu"taxon:9606"
/cloneu"IMAGE:1505684"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.2%; Score 147; 99.6%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGTTAAAATAAAAATCAGTATGATGG 1
location/Qualifiers
                                                                                                                                                   /lab_host="DH10B"
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins , M., Willman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Saares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                            1724 AGGTTGAGGAGGGAGGATGGCTTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACATAAC 1783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
MARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should bept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO74342 Linear EST 23-DEC-199
zml5g03.sl Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:525748 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                      DB 10; Length 364;
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/db_xref="GDB:3917177"
/db_xref="taxon:9606"
/db_xref="HAGE:525748"
/clone="IMAGE:525748"
/clone_lib="Stratagene pancreas (#937208)"
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                                                                                                                                                                                                                           100.0%; Preu ...
                                                                                                                                                                                                         Score 85;
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AAO74342.1 GI:1614210
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                                                                                                                                                                                                                                                                85; Conservative
                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: capabs.rfemail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 354.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.6%; Score 101; DB 12; Length 1140;
100.0%; Pred. No. 0;
tive 0; Mismatches 0; Indels 0
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/db_xref="taxon:9606"
                                                                                    /organism="Homo sapiens"
High quality sequence stop: 635.
                           Location/Qualifiers
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Note: til.
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Unpublished (1997)
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                                                            source
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KEYWORDS
SOURCE
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RESULT 41 BE898834/c

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DEFINITION

ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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Eucharders (Craniata; Vertebrata; Euteleostom1; Eucharders (Craniata; Vertebrata; Euteleostom1; Eucharderia; Eucharderia; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eucharderia; Primates; Catarrhini; Hominidae; Homo.

Man, 1. (100.) (Man, 100.) (Man, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 bp mRNA linear EST 05-JUN-2000 RC5-BN0158-190400-031-G01 BN0158 Homo sapiens CDNA, mRNA sequence. BE008586 BE008586.1 GI:8268819
                                                       AV719004 GLC Homo sapiens CDNA clone GLCEJB05 5', mRNA sequence.
AV719004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dias Nato, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsıkuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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/db_xref="taxon:9606"
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Mammalia; Eutheria;
1 (bases 1 to 252)
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RESULT 42
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/Clone_Inb="NIH_MGC_9".
/Lissue_type="adenocarcinoma cell line"
/Lab_host="bH10B (phage=resistant)"
/Lab_host="bH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 878)

S NIH-MCC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DorD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCWR21 row: p column: 05

High quality sequence stop: 783.

Location/Qualifiers

Lrce

1. 878
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                                                                                                                                                                                                                                           1983 GCACCTGTAATCCCAGGTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGG 2042
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0;
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                        2.6%; Score 73; DB
100.0%; Pred. No. 0;
iive 0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:3952372"
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                                                                                                                   Best Local Similarity 100.
Matches 73; Conservative
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Best Local Similarity
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                                                                                 Query Match
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BASE COUNT ORIGIN

Matches

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Gaps 0;

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Tumor Gene Index
Institute, Cancer Senome Anacomy Figure (Cont.)
Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Preparation: David B. Consortium/LNL at:
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: 590 Std Error: 0.00
Seq primer: -40ml3 fdw. Erf from Amersham
High quality sequence stop: 296.
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AA548692
AA548692.1 GI:2318974
EST.
                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN1058"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18: Site_l: Smal;
Site_2: Smal; A min1-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
1986 CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGG 2045
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 318)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 253; 0;
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Location/Qualifiers
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                                                                                                                                                              Seq primer: puc 18 forward
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/organism="Homo
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Best Local Similarity
Matches 70; Conserv
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                                                                                                                                                                             Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC5-BN0158-190
400-031-G01&t3=2000-04-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 bp mRNA linear EST 05-JUN-2000 RC5-BNI058-020500-031-G01 BN1058 Homo sapiens cDNA, mRNA sequence. BED12103.1 GI:8272336 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: Dreast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G. S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                             Contact: Simpson A.J.G.
Laboratory of Gancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
  Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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100.0%; Pred. No. v,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0158"
//dev_stage="Adult"
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                                                                                                                                                            Tel: +55-11-2704922
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Best Local Similarity 100.0
Matches 70; Conservative
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 146 AGGTTGCAGT 155
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Best Local Similarity
Matches 70; Conserva
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordatas; Catarrhini; Hominidae; Homo.

1 (bases 1 to 334)
Gu,J.; Zhao,M.; Huang,Q.; Xu,X.; Li,Y.; Peng,Y.; Song,H.; Xiao,H.;
Gu,Y.; Li,N.; Qian,B.; Liu,F.; Qu,J.; Gao,X.; Cheng,Z.; Xu,Z.; Zeng,Y.; Gao,W.; Tu,Y.; Jia,J.; Fu,G.; Ren,S.; Zhong,M.; Lu,G.; Yang,Y.; Gao,G.; Zhang,Q.; Chen,S.; Han,Z.; and Chen,Z.; Lu,G.; Unpublished (2000)
                                                                                                                                                                                                                                                            AV759459 MDS Homo sapiens cDNA clone MDSARB02 5', mRNA sequence.
AV759459 MDS GI:10917307
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                                                           /note="Organ: prostate; Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
103 c 93 g 71 t
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/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
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                              /tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
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Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Banil: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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/clone_lib="NCI_CGAP_Pr11"
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/db_xref="taxon:9606"
/clone="MDSARB02"
                                                                                                                                               70 9
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                 /sex-"male"
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Best Local Similarity
Matches 70; Conserv
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Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases I to 448)

1 (bases I to 448)

1 (bases I to 448)

2 (chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hullman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags 97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N22395 448 bp mRNA linear EST 20-DEC-1995 yw37f08.sl Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:254439 3' similar to contains Alu repetitive element; , mRNA
                                     Clones are available from Research Genetics (info@resgen.com). BAC end search page:
end search page:
trp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Ml3-21
class: BAC ends.
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 844 Std Error: 0.00
Seq primer: m13 -40 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17; Length 437,
0;
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0; Mismatches
                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="233917"
/clone_lib="CIT-HSP"
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/db_xref="GDB:3891892"
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                     Email: mdadams@tigr.org
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N22395.1 GI:1128529
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Matches 70; Conservative
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Fax: 301 838 0208
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1 (Dases I to 437)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
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              Eukaryottani Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 346)

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,M., Shen,K., Lu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z., and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Tel: 86-21-50801912
Email: hanzgépac.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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/dev_stage="Adult"
/lab_host="SOLR"
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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100.0%; Pred. No. 0;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCAUD05"
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Unpublished (1998)
Other_GSSs: CIT-HSP-233917.TR
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AQ056722.1 GI:3353328
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HS_5569_B2_F07_SP6_RPCI-11 Human Male_BAC_Library Homo sapiens genomic clone Plate**1145 Col***14 Row**L, DNA sequence.

AQ741937.1 GI:5519459
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Butazyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 642)

2 (based, A. I., Shernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, J. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.
                                                                                                                                                                             Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray inpublished (2000).

Contact: John Quackenbush The Institute for Genomic Research The Institute for Genomic Rockville, MD 20850, USA PTI: 301 838 3528 Fax: 301 838 0208
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red. No. 0;
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; P.
Matches 70; Conservative 0;
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AW973278.1 GI:8163144
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Plate: 316
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/db_xref="taxon:9606"
/clone="IMAGE:554439"
/clone="IMAGE:554439"
/clone="IMAGE:554439"
/clone="IMAGE:554439"
/clone="IMAGE="Morton Fetal Cochlea"
/dev_stage="16-22 week fetus"
/dev_stage="16-22 week fetus"
/dev_stage="16-22 week fetus"
/dev_stage="16-22 week fetus"
/dev_organ: ear; Vector: pBluescript SK-; Site_1: EcoRI;
/note="Organ: ear; Vector: pBluescript SK-; Site_1: EcoRI;
Site_2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
unidirectionally. Primer: Oligo dr. Fetal cochlea, normal.
37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni: ZAP
XR Vector: Library constructed by N. Robertson, C. Morton.
-5' adaptor sequence: 5' GAATTGGGAGGG 3' -3' adaptor
sequence: 5' CTCGAGGGG 3' -3' adaptor
sequence: 5' CTCGAGGGG 3' -3' adaptor
122 t 3 others
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Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eutheria: Eutheria: Primates; Catarrhin1: Hominidae: Homo.

I (bases 1 to 544)

S Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,

Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ284662 544 bp DNA linear GSS 04-MAY-1999
RPCI11-7809.TV RPCI-11 Homo sapiens genomic clone RPCI-11-7809, DNA
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Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please context Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: T7

Class: BAC ends.
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI:
RPCIII Human Male BAC Library"
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/clone_lib="RPCI-11"
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AQ284662
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 571)

S Adams,M.D., Kelley,J.M., Rounsley,S.R. and Venter,J.C.
Use of a BAC End Sequence Database for Sequence-Ready Map Building Unpublished (1997)

Other_GSSs: 837A4_TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdddams@tigr.org
Elones are available from Research Genetics (info@resgen.com). BAC
        Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Direct Submission
Chamical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@gac.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B14085 S71 bp DNA linear GSS 18-JUN-1998
A-837A4.TP CIT978SK Homo sapiens genomic clone A-837A4, DNA
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Seq primer: SP6
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
a 138 c 148 g 175 t 4 others
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/organism="Pan troglodytes"
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/clone="RP43-060A09.TJ"
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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R.Site 1 : ECORI
R.Site 2 : ECORI.
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B14085.1 GI:2121834
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_ilb="ReCI-11 Human Male BAC Library"
/sax="male"
/sax="male"
/sote="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

58 a 88 c 153 g 150 t
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1 (bases 1 to 649)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Reller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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Pan troglodytes
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                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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Pan troglodytes DNA, clone: RP43-060A09.TJ, genomic survey
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Seq primer: SP6
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  Homo sapiens
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Fri Jul 18 09:29:38 2003

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Raap, A.K., Morley, M. and Bruzel, A.

Raap, A.K., Morley, M. and Bruzel, A.

A resource of mapped human bacterial artificial chromosome clones

A resource of mapped human bacterial artificial chromosome clones

Concome Res. 9 (10), 989-993 (1999)

B 99455100

On Dec 1, 2000 this sequence version replaced gi:10183605.

Contact: Arcaro MA, Morley M, Burdick J, Cheung VG

Department of Pediatrics

University of Pennsylvania
3516 Civic center Blvd, ARC 516, Philadelphia, PA 19104, USA

Tel: 215 590 2664

Fax: 215 590 3709

Email: mlennox@mail.med.upenn.edu

Plate: 436 row: N column: 15

Seq primer: SP6

Class: BAC ends.
                                                                                                                                                                                                                                                      AZ303190 397 bp DNA linear GSS 01-DEC-2000 UP_436-15N_SP6 RPCI11 Human Male BAC Library Homo sapiens genomic clone RPI1-436NI5, DNA sequence.
                            1986 CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGG 2045
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                                                 205 CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAAATCGCTTGAACCCAGGAGGTGC 264
                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_libu"RPCII1 Human Male BAC Library"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; RPCI11 Human Male BAC Library"
. 81 c 121 g 69 t
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Primates; Catarrhini; Hominidae; Homo.
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/db_xrefe"taxon:9606"
/clone="RP11-436N15"
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Mammalia; Eutheria;
1 (bases 1 to 397)
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Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;

Mammalia: Butharia: Primates: Catarrhini: Hominidae: Homo.

1 (Dases 1 to 300)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready Map Building

Unpublished (1998)

Other GSSs: CITBI-E1-2521L5.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208
1. .571
/organism="Homo sapiens"
/db_xref="taxon:9666"
/db_xref="taxon:9666"
/clone="A-837A#
/clone="Ib="CIT9788K"
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/sex="Female"
/coll_type="Fibroblast"
/note="vector: PAC108L; Site_1: HindIII; Site_2: HindIII;
CalTech Human BAC Library A"
/calTech Human BAC Library A"
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                                                                                                                                                                                                                                                                                                                                   1987 CTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAATCGCTTGAACCCAGGAGGTGGA 2046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
66 c 84 g 58 t
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/db_xref="taxon:9606"
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1. .300
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AQ276581.1 GI:3902777
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AQ276581
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AQ750497 LC06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1152 Col=11 Row=F, DNA sequence.
AQ750497.1 GI:5537655
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please context Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphocytes"
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RPCIll Human Male BAC Library"
157 c 212 g 129 t
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Clones are derived from the human BAC library RPCI-11. For BAC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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Pred. No. 0;
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University of Washington
VOID Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
                                                                              Mark Adams
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                                                                                                                                                   20850
                        Unpublished (1997)
Other GSSS: RPCI-11-248K21.TJ
Other GSSS: RPCI-11-248K21.TJ
Contact: Shaying Zhao, William Nierman, Ma.
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 208:
Tel: 301 838 0200
Fax: 301 838 0200
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High Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:7595108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
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/clone_lib="RPCI-11"
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1. .725
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Matches 67; Conservative
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       Map Building
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/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: marrow: Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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RPCI-11-248K21.TV RPCI-11 Homo sapiens genomic clone RPCI-11-248K21
AQ478179
                                                                    Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelara, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpsonedudwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-MT0246-190101-811-d10&t3=2001-01-19&t4=1)
Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 483)
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                                                                                                                                                                                                                                                                                                                                    Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                Shorgun sequencing of the human transcriptome with ORF expressed
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20202663
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0;
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100.0%; Pred. No. 0;
tive 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 470.
Location/Qualiflers
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
1 (bases 1 to 725)
                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Fax: +55-11-2707001
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AW882256
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 286)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagali,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deolivelre,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC5-OT0055-080 300-021-C12&t3=2000-03-08&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
                                                                                                                                                                                                                    /organism="Homo sapiens"
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100.0%; Pred. No. 0;
Live 0; Mismatches 0; Indels
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                                                                               http://www.htsc.washington.edu
Plate: 1152 row: F column: 11
Seq primer: T7
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High quality sequence stop: 286
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Location/Qualifiers
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Fax: +55-11-2707001
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Matches 67; Conservative
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/note="Organ: Ovary; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions. 59 t
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1 (bases 1 to 286)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brioncs,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Bruntein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl.et2 RC5-OT0055-080
300-O21-Dl06t3=2000-03-086t4")
Seq primer: puc 18 forward
High quality sequence stops: 286.
Location/Qualifiers
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/dev_stage="Adult"
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
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Pred. No. 0;
0; Mismatches 0; Indels
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Laboratory of Cancer Genetics
                                                                 /clone_lib="OT0055"
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124 AGGTTG 129
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1 (bases 1 to 286)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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/note="Organ: ovary: Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC5-OT0055-080 300-021-E12&t3=2000-03-08&t4=1)
Seq primer: puc 18 forward High quality sequence stop: 286.
Location/Qualifiers
from ORESTES PCR (U.S. Letters Patent application No. 196 7716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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tive 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Smal; A mini-llbrary was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

94 a 62 c 71 g 59 t
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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asinpson@ludwig.org.br

Project. This sequence with a second from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2eRC5-OT0055-080

300-021-F128513-2000-03-08&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 286.
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                                                                                                         1986 CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGAGAATCGCTTGAACCCAGGAGGTGG 2045
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                         Gaps
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20202663
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butaryota Eutheria; Primates; Catarrhini; Hominidae; Homo. (a. 1 (bases 1 to 402) (b. 1 (b. 1 (b. (b.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are available from Research Genetics (info@resqen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: M13 Reverse class: BAC ends.
         Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Reudy Mup Building
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII: Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 2.3%; Score 66; DB 17; Length 395; Best Local Similarity 100.0%; Pred. No. 0; Matches 66; Conservative 0; Mismatches 0; Indels
                                                                                                                                                Unpublished (1997)
Other GSSs: CIT-HSP-2006D8.TFB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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AA679794/c
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Nashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
Image.llnl.gov/image/html/iresources.shtml
Seq primer: -40Up from Gibco
High quality sequence stop: 382.
Location/Qualifiers
I. .388
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//db_xref="taxon:9606"
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//tlssue_type="lymphoma, follicular mixed small and large
//lsh host=lymlon"
                                                                                                                                                                                              xx65h01.x1 NCI_CGAP_Lyml2 Homo sapiens cDNA clone IMAGE:2848561 3' similar to contains Alu repetitive element;, mRNA sequence.
AW518030 GI:7156112
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//note="Organ:.lymph node; Vector: pCMV-SPORT6; Site_1:
Sal1; Site_2: NotI; Cloned unidirectionally. Primer:
Sal2; Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
107 c 76 q 96 t 1 others
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 395)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 430)
S Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)
Unpublished (1998)
Cottact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                     1986 CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGG 2045
                                                                                                                                                                                                                                                                                                                                                                                                                            AQ111323 AQ11-198 DNA linear GSS 29-AUG-1998 CIT-HSP-2371K16.TR CIT-HSP Homo sapiens genomic clone 2371K16, DNA
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/cell_type="Fibroblast"
/note="Vector: pBAC108t, Site_1: HindIII; Site_2: HindIII;
/note="Wector: pBAC108t, A"
calrech Human BAC Library A"
1 102 c 95 g 120 t
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Ml3 Reverse
Class: BAC ends.
                                                                                                                                                                                                                          /cell_type="Sperm"
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                                                                                                                     2.3%; Score 66; DB 17; Length 414;
100.0%; Pred. No. 0;
Live 0; Mismatches 0; Indels
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100.0%; Pred. No. 0;
tive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
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AQ111323.1 GI:3487980
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                                                                                                                   Query Match 2.35
Best Local Similarity 100.0
Matches 66; Conservative
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S Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Kim, U.-J., Shizuya, H., Simon, M. and Venter, J.C.
Use of a human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1997)
Other_GSS: CIP978SK-A-699D2.TVB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B72122 414 bp DNA linear GSS 18-JUN-1998 CIT978SK-A-699D2.TPC CIT978SK HOMO Sapiens genomic clone A-699D2,
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 339.
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0
                                                                                              /organism="Homo sapiens"
/db_xref="taxon:966"
/clone="IMAGE:1141919"
/dev_stage="hNT neuron (#937233)"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                         Length 402;
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100.0%; Pred. No. 0;
tive 0; Mismatches (
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/clone_lb="CIT978SK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Matches 66; Conserv
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 526)

1 (bases 1 to 526)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 National Institutes of Health, Mammalian Gene Collection (MGC)

5 Unpublished (1999)

5 Other_ESTS: ba84g06.y1

6 Contact: Robert Strausberg, Ph.D.

7 Email: cgapbs-r@mail.nih.gov

7 Tissue Procurement: ATCC

7 CDNA Library Preparation: Ling Hong/Rubin Laboratory

7 CDNA Library Arrayaed by: The I.M.A.G.E. Consortium (LIML)

8 DNA Sequencing by: Washington University Genome Sequencing Conter
                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE301068 526 bp mRNA linear EST 14-JUL-2000 ba84906.xl NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2907130 3' similar to contains Alu repetitive element;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: ovary: Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor; papillary serous, clear cell, spindle cell. Al are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 451)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NALional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/clone="IMAGE:2216520"
/clone_lib="NCI_CGAP_Ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host-"DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.3%; Score 66; DB 9; Length 451; llarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1185 Std Brror: 0.00
Seg primer: -400p from Gibco
High quality sequence stop: 417.
Location/Qualifiers
                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 g
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1 (bases 1 to 434)
Mahalas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                             AQ878262 434 bp DNA linear GSS 09-NOV-1999 HS_2272_B2_C10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2272 Col=20 Row=F, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High Throughput Esquencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). Blate: 2272 row: F column: 20 Seq prime: 77
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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/db_xref="taxon:9606"
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/note="Organ: head_neck; Vector: pucl8; Site_1: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

79 c 115 g 84 t
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Mammalia; Butheria; Primates; Catarrhini; Hominidae: Homo.

1 (bases 1 to 400)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=0V0.HT0368-310
100-091-c078t3=2000-01-31&t4=1)
Seq primer: puc 18 forward
High quality sequence strar: 9
High quality sequence stop: 400.
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/note="Organ: head_neck; Vector: puc18; Site_1: Smal:
Site_2: Smal; A mini-library was made by cloning products
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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100.0%; Pred. No. v.
... 0; Mismatches
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0368"
/dev_stage="Adult"
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/clone_lib="HT0368"
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BE156526.1 GI:8619247
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/clone_IIb="NIH_MGC_21"
/tlone_Lib="Choriocarcinoma"
/lab_host="Choriocarcinoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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BE156416.1 GI:8619137
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1 (bases 1 to 395)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVO-HT0368-030 100-080-ci2&t3=2000-01-03&t4=1)
Seq primer: puc 18 forward
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
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found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -400p from Glbco
High quality sequence stop: 441.
Location/Qualifiers
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/db_xref="taxon:9606"
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Location/Qualifiers
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Fax: +55-11-2707001
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Matches 66; Conserv
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Query Match
Best Local Similarity 100.(
Matches 65, Conservative
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dcone_lib="urgood4"
/dev_stage="Adult"
/note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196.716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 443)

Diass Neto.E., Garcia, Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-270701

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3.UT0034-170

800-012-hl0&t3=2000-08-17&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 176.
  derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) poffiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
                                                                                                                                                                   DB 10; Length 400;
0;
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                                                                                                                                                                       ch 2.3%; Score 65; DB Similarity 100.0%; Pred. No. 0; 65; Conservative 0; Mismatches
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90 c 134 g 87
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BE940056.1 GI:10469142
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Eukaryota: Metazoa: Chordata; Cranlata; Vertebrata; Euleleostomi; Eukaryota: Metazoa: Chordata; Cranlata; Vertebrata; Euleleostomi; Mammalia; Eurheria: Primates; Catarrhini; Hominidae: Homo.

1 (bases 1 to 573)

8 Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 301 838 0200
Email: hoe@tigr.org
Clones are derived from the human BAC library RPCI-II. For BAC
                                                                                                      2037
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RPCII1-110D15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-110D15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library availability, please contact Pleter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (inf@tessen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
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Pred. No. 0;
0; Mismatches
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/db_xref⇔"GDB:7541942"
/db_xref↔"taxon:9606"
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/clone_lib:="RPCI-11"
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100.0%; Pre
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AQ318054.1 GI:4051349
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RESULT 77

us-09-966-880a-7.100olig.rst

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 47N).

1 (hases 1 to 47N).

2 Hillar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Willamson, A., Wohldman, P. and Wilson, R.

The Washu Merck EST Project

L Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAG
                                                                                                                                                                           Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please context Peter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
a 100 c 134 g 115 t
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1979 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAG
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Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 64; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/db_xref="GDB:7551409"
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High quality sequence stop: 357
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa: Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 468)

NGI/NINDS-CAP http://www.ncbi.nlm.nlh.gov/ncicgap.

NGI/NINDS-CAP http://www.ncbi.nlm.nlh.gov/ncicgap.

NGI/NINDS-CAP http://www.ncbi.nlm.nlh.gov/ncicgap.

NGI/NINDS-CAP http://www.ncbi.nlm.nlh.gov/ncicgap.

NGI/NINDS-CAP http://www.ncbi.nlm.nlh.gov/ncicgap.

AL Unpublished (1998)

Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-rfmail.nlh.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGI-CASP clone distribution information can be
                        BG059756 MRNA linear EST 25-JAN-2001 marks linear EST 25-JAN-2001 marf5205.x1 NCI_CGAP_Brn65 Homo sapiens cDNA clone IMAGE:4147593 3' similar to contains Alu repetitive element;, mRNA sequence. BG059756
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RPCII1-13402.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-13402,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 470)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .468
/organism="Homo sapiens"
/db_xref="Laxon:9606"
/clone="IMAGE:4147593"
/clone="Lib="NGI_CGAP_BENGS"
/tissue_type="glioblastoma without EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pGWY-SPORTS; site_1: NotI;
Site_2: Sali; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.77 kb. Constructed by Life
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2.3%; Score 64; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 64; Conservative 0; Mismatches
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Seg primer: -40UP from Gibco
High quality sequence stop: 416.
Location/Qualifiers
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yadd, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (12-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC):

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9110)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                 1979 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTTGAACCCAG 2038
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Pan troglodytes
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Pan troglodytes DNA, clone: PTB-019B13.R, genomic survey sequence.
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                                                                                       /sex="Male"
/call_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCIII_Human Male BAC Library"
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TotoKi,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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/clone_lib="PTB Chimpanzee Male BAC Library"
174 c 157 g 193 t 1 others
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Mismatches
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     /db_xref:"taxon:9606"
/clone="RPCI-11-259A5"
/clone_lib="RPCI-11"
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/clone="PTB-019B13.R"
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1 (bases 1 to 657)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
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Other_GSSS: RPCI-11-259A5.TJ
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Other_GSSS: RPCI-11-259A5.TJ
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Other_GSSS: RPCI-11-259A5.TJ
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fea: 301 838 0200
Fea: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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                                                    /organism="Homo sapiens"
/db_xref="GDB:3792513"
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/db_xref="GDB:7599076"
                                                                                                        /db_xref="taxon:9606"
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AQ480012
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Best Local Similarity
Matches 64; Conserv
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AQ480012
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BF933309.1 GI:12350633
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Matches 63;
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Unpublished (1997)
Other_GSSs: RPC1-11-195F6.TV
Contact: Shaying Zhao
Contact: Shaying Labo
Contact: Shaying Labo
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: John Carlone Toom the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@delong.med.buffalo.edu. Clones may be purchased from
BACFAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
This BAC end was generated during the R&D process and may have
                                                                                                                                                                                         AZ516708 263 bp DNA linear GSS 16-OCT-2000 RPCI-11-195F6.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-195F6,
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1979 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAG 2038
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 263)
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
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100.0%; Pred. No. 0;
ive 0; Mismatches
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/organism="Homo sapiens"
/db_xref="GDB.7574611"
/db_xref="taxon:9606"
/clone_lib="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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A2516708
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BF933309/c
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424 bp mRNA linear EST 15-DEC-1999 tw79ell.xl NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2265932 3' similar to contains Alu repetitive element; contains element THR repetitive element;, mRNA sequence.
AI673749.1 GI:4853480
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 380)
Dias Neto. E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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/dev_steage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-NT0273-201200-356-92080-12-2000-112-20844=1)
Seq primer: puc 18 forward
High quality sequence stop: 342.
BF933309 380 bp mRNA linear EST 22-JAN-2001
LL5-NT0273-201200-369-e03 NT0273 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae: Homo.

1. (bases I to 454)

2. Admas, M.D.; Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Orber_GSS: RPCIII-69015.TK

Contact: Mark Adams

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Fax: 301 838 0206
Fax: 301 838 0206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are derived from the human BAC library RPC1-1]. For BAC
Library availability, please contact Pieter de Jonq
(pieter@dejong.med.buffalo.edu.). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type."Lymphocytes"
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RPCIII Human Male BAC Library"
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/organism~"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref~"taxon:9606"
/clone~"RPCI-11-70N2"
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AQ268452
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                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-refamil.nih.gov

Tisque Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.linl.gov/bbrp/image/image.html

Insert Length: 2630 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop:

Location/Qualifiers
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I (bases 1 to 445)

S Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1979 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAG 2038
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RPCI11-70N2.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-70N2, DNA
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                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 424)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_lib="NCI_CGAP_Ut3"
/fissue_type="poorly-differentiated endometrial adenocarcinoms, 2 pooled tumors"
/lab_host="DH108"
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/db_xref="taxon:9606"
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/sex="male"
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1. .502
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AQ624960
AQ624960.1 GI:5087352
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1 (bases 1 to 490)

1 (bases 1 to 490)

2 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

1 Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

1 Unpublished (1998)

1 Other_GSSs: CITHESP-2306J3.TR

Contact: Mark Adams

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Tel: 301 838 0200

Fax: 301 838 0200
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                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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      /clone="RPCT-11-69015"
/clone_lib="RPCT-11"
/sex="Wale"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
1 98 c 102 g 85 t
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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/db_xref="taxon:9606"
/clone="2306J3"
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/db_xref="taxon:9606"
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1993 TCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGC 2052

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Contract: Shaying Languages; Cacatilliul; Hominidae; Homo.

Shao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.

Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

Unpublished (1997)

Other_CSS: CITRIE-E1-2649E20.TR

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Tel: 301 838 0200

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
                                                                                                                                                                                                               AQ624960 502 bp DNA linear GSS 16-JUN-1999 CITBI-E1-2649E20.TF CITBI-E1 Homo sapiens genomic clone 2649E20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Ml3-21
Class: BAC ends.
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/note="vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
123 q 129 t
98
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0;
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100.0%; Pred. No. 0;
tive 0; Mismatches
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/db_xref="taxon:9606"
/clone="2649E20"
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ACCESSION
VERSION
KEYWORDS
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AL042927

T16 bp mRNA linear EST 29-FEB-2000
DKFZp434K1322_s1 434 (synonym: htes3) Homo saplens cDNA clone
DKFZp434K1322 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2): Email s.wiemann@dkfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Blum, H.; Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Blum, et al.)
Unpublished (1999)
    Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.dc; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp686D2029) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GFRMANY; Email: clone@tzpd.de.
                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfilB;
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Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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This clone (DKFzp434K1322) is available at the R2PD in Berlin.
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/db_xref="taxon:9606"
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/tissue_type="testis"
/tasue_type="adult"
/lab_nost="DH10B"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
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0;
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/clone="DkFzp686D2029"
/clone=lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
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                                                                                                                                                                                                                                                                                                                                                                                                                    163
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/lab_host="DH10B"
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AL042927.1 GI:5422360
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Best Local Similarity
Matches 63; Conserv.
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                                                                                                                                                                                                                                                                                Submitted (02-AUG-2001) Asao Fullyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehitro-chour Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1993 TCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGC 2052
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DKEZp686D2029_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKEZp686D2029 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 683)
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
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Fullyama. A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
                                                                                                       Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watenabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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0
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/clone_lib="PTB Chimpanzee Male BAC Library"
132 c 141 q 154 t
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-138L16.F"
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Library clone: PTB-138L16.F.
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Unpublished (1999)
Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
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                       troglodytes
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Best Local Similarity
Matches 63; Conserv
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SOURCE

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Eukaryota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi; Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini: Hominidae: Homo.

1 (bases 1 to 1034)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The II.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the II.M.A.G.E. Consortium/LLNL at:

Http://mage.llnl.gov

Plate: LLCM1695 row: e_column: 04
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                                                                                  BG755005 1034 bp mRNA linear EST 15-MAY-2001 602711511F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851819 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="minary" broals from tonsils (cell line)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Size_selected >500bp for average insert size 1.8kb. Library constructed by Lin Hong in the laboratory of Gerald M. Rubin (University of California, Berkels) using ZAP-CDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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100.0%; Pred. No. v,
... 0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:4851819"
/clone_lib="NIH MGC_48"
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Location/Qualifiers
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/clone="lthanGE:6301509",
/clone=lib="NHLMGC_113"
/lab_host="bH10B (phage-resistant)"
/ncl="Corgan: spleen; Vector: pOTBT; Site_1: XhoI; Site_2:
ECRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ707295 734 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8475232 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6301509
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(Dases 1 to 734)

NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                  Length 716;
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/organism="Homo sapiens"
/db_xref="taxon:9606",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.rdmail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.lnl.gov
The following repetitive elements were found in this CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 308)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria;
1 (bases 1 to 396)
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/tissue_type="succionidial none
/dev_stage="Addit"
/lab_host="Dilo" (Life Technologies)"
/lab_host="Dilo" (Life Technologies)"
/lab_host="Dilo" (Life Technologies)"
/note="Organ: Bone: Vector: pTT3-pac (Pharmacia) with a modified polylinker; Site_1: EcoR I: Site_2: Not 1:
NCI_CGAP_DF0 is a cDNA library containing the following tissue(s): Subchondral Bone: The library was constructed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pTT73-pac vector. The oligonucleoctide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) R tall. The man the Not I site and the (dT) R tall. The
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: 1249 Std Error: 0.00
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
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()
                                                                                                                                                                                                                    /clone="IMAGE: 3108204"
/clone_lib-"NCI_CGAP_DF0"
/tissue_type="Subchondral Bone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_LIB=UI-H-DF0
TAG_TISSUE-subchondral bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                          /organism~"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.2%; Score 61;
                                                                                                                                                                                    /db_xref-"taxon:9606
                                                                                                Location/Qualifiers
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>MER5A#DNA/MERI_type
Seq primer: M13 FORWARD
POLYA=Yes.
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 61; Conserval
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RPCI-11-194F22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-194F22 A0414005
                                                              /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                  1995 CCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAG 2054
                                                                                                                                                                                                                                                                                                                                                         Email: hbe@tigr.corg
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Resparch Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Macriat 1997)

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
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O
                                                                                                                                                                                                                                          2.2%; Score 61; DB 17; Length 404;
100.0%; Pred. No. 0;
tive 0; Mismatches 0; Indels
/clone="Plate=767 Col=23 Row=G" /clone_lib="RPCI-11 Human Male BAC Library"
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/cell_type="Lymphocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="RPCI-11-194F22"
/clone_lib="RPCI-11"
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                                           /sex="male"
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Mammalia; Eutheria;
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Best Local Similarity 100.(
Matches 61; Conservative
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KEYWORDS
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Fax: (206) 616-3887
Email: jWallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 767 row: G column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS_5191_Al_D12_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=767 Col=23 Row=G, DNA sequence.
                                                                                                                                                                                                                                                             tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 404)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pAMP10; mRNA made from invasive ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 400;
0;
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Seg primer: -40ml3 fwd. ET from Amersham
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100.0%; Pred. No. v,
... 0; Mismatches
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                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:1385551"
/clone_lib="NCI_CGAP_Ov2"
/sex="female"
                                                              1. .400
/organism="Homo sapiens"
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                  High quality sequence stop: 353.
Location/Qualifiers
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Location/Qualifiers
                                                                                                                                                                                            /tissue_type="ovary"
/lab_host="DH10B"
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Class: BAC ends
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, DNA sequence.
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pleter@deJong med.buffalo.edu, Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
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1 (bases 1 to 460)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
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Use of BAC End Sequences from Library RPC1-11 for Sequence-Ready Map Building
Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 301 838 0200
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Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; H
1 (bases 1 to 498)
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ACCESSION KEYWORDS SOURCE

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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
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Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1c-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus sphice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 25, 2002 this sequence version replaced gi:20901754. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (18-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                      Submitted (25-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department
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Submitted (25-MAY-2002) Human Genome Sequencing Center, Departmen
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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/clone="RP11-438L7"
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Eukaryota; Madams, C., Addro-Oduola, B., Ali-osman, F.R., Allen, C., Alsuyo, D.M., Adams, C., Addro-Oduola, B., Ali-osman, F.R., Allen, C., Alsuyo, D.M., Adams, C., Addro-Oduola, B., Ali-osman, F.R., Bluna, C., Alsuyo, D.M., Burch, D., Bryd, N.C., Carron, F.R., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chavez, D., Chanez, C., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Carton, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Carron, F.R., Delgado, D., Barder, D., Dathenre, S.R., David, R., Delgado, D., Edward, S., Dubin, H.H., Davis, C., Davy, Carroll, L., Dederich, D. A., Delaney, K.R., Delgado, D., Edward, C., Endri, J., Chin, S., Carter, D., Edward, C., Edward, J., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunzarene, P., Hale, S., Hanes, A., Harnandez, J., Harris, C., Harris, C., Harris, K., Hart, M., Havlak, P., Hamallton, K., Han, J., Harris, C., Harris, K., Hart, M., Haylak, P., Hune, J., Ioshikke, I., Jackson, L.E., Jacobson, B., Jia, Y., Lucier, K., Holloway, C., Hollins, B., Homis, F., Howard, S., Huber, J., Lucier, R., Luu, W., Loulseged, H., Lozado, R.J., Lu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, M., Loulseged, H., Lozado, R.J., Lu, M., Mapus, P., Martiney, E., So
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                                                                                             742 TCCTTCAAGTCTTCTCTGTTTTTATTCTTCAACTCTCACTTTCTTAGAGTTTACAGAAA
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BC006296 1837 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, activation-induced cytidine deaminase, clone MGC:12911 IMAGE:4054915, mRNA, complete cds.
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DFGYLRNKNGCHVELLFLRYISDWDLDDGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRIGL"
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Contact: nisc_mgc@hipgi.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Boulfard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho.S.-L., Karlins,E., Laguspi.R.,
Lim,M., Wanduro,O.L., Maslello,C., Mastrian,S.D., Mc(loskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA qi: 9988409.
                                                                                                                                                                                                                                                                                                               Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: MGC help desk maintenance: MGC help desk mail: egabbs refmail.nih.govu trissue Procurement: Louis Staudt cDNA Library Preparation: Rubin Laboratory DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.) DNA Sequencing by: National Institutes of Health Instrumural Sequencing Center (NISC).
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Catarrhini; Hominidae; Homo.
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/product"=activation-induced cytidine deaminase"
/product=in_id="AANH06296.1"
/db_xref="GI:13623401"
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/tissue_type:"Primary B-Cells from Tonsils"
/clone_lib:"NIH_MGC_48"
/lab_host."DH10B-R"
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/db_xref."LocusID:57379"
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Mammalia, Eutheria, Primates,
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Web site: http://
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                            CACAGGAAAACTTGAATGCACAACTGTCTTATTTTAATCTTATTGTACATAAGTTTGTAA
             TTAACTATATAAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACACG
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                                                                              CTCATAGTTCTAGCTGCTTGGGAGGTTGAGGAGGGAGGATGGCTTGAACACAGGTGTTCA
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Martin, A. and Scharff, M.D.
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Martin, A. and Scharff, M.
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Eukaryota; Metazoa;
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AWEGLHENSVRLZGURRILLPLYEVDDLRDAFRTLGL"
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2 (bases 1 to 596)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
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1. .596
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NLSLAFFARLYFCEDRRAEPBGLRRLHRAGYOIAIMTFKDYFYCWNTFVENHERTFK
AWBGLHENSVRLSRQLRRILLDLYFVDDLRDAFRTLGL"
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Homo sapiens clone Ramos 9 AID (Alb) mRNA, partial cds.
AF529823
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Submitted (17-JUL-2002) Cell Biology, Albert Einstein
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
                                                                                                                                                                                                                                                          AID transgene in B cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 596
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Pred. No. 4.5e-293;
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/clone."Ramos 9"
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/gene-"AID"
/note="integrated into
                                                                                                                                                                                          Primates;
                                                                                                                                                                      Chordata;
                                                                                                                                                                                                                                                          Somatic hypermutation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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9 ò q à qq ò g

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AF529842 597 bp mRNA linear SYN 19-AUG-2002
Cricetulus griseus clone 2 transgenic Homo sapiens AID (AID) mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                  TTACTGCTGGAATACTTTTGTAGAAACCATGAAAGTTTTCAAAGCCTGGGAAGGCT 494
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
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10461, USA
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TTACTGCTGGAATACTTTTGTAGAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCT
                                                                                                       274 CTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAG
                                                                                                                       CCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAG
                                                                                                                                                                                                                               TCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCCGAGGG
                                                                                                                                                                                                                                                                                          GCTGCGGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTT
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                                              CTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACAT
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Submitted (17-JUL-2002) Cell Biology, Albert Einstein
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
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/db_xref="taxon:10029"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens"
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/db_xref="taxon:9606"
1. .597
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Martin, A. and Scharff, M.D.
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Eukaryota, Metazoa;
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAINTFKDYFYCWNTFVENHERTFK
WEGLHENSYLSRQLIALLFLYFVDDLRDAFRTWGR"
165 c 157 g 147 t
                                                                                                                                                                                                                                                                          AF529846 19-AUG-2002 Cricetulus griseus clone 6 transgenic Homo sapiens AID (AID) mRNA,
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                 432
                                              571
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                                                                                                         CTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTTTTGCCCCTGTAT 631
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                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Cricetinae;
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (101-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-B
 TTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGG
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B cells and
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Pred No. 8.2e-287;
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/db_xref="taxon:10029"
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larity 100.0%; Pred. No. 8.2
Conservative 0; Mismatches
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/db_xref="GI:22297280"
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/db_xref="taxon:9606"
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Rodentia;
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1. .597
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/cell_line="CHO"
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/product="AID"
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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2 (bases 1 to 597)
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AF529846
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les 572; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 Cricetulus.
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                                                                                                                                       493
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                                                                                                                                                                                                                                                                                          DEFINITION
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AUTHORS
TITLE
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KEYWORDS
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/protein_ld-"AAM95434.1"
/brotein_ld-"AAM95434.1"
/box.xref="dol:22297282"
/translation-"MDSLLMNRRFIVOFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DFGYLNNKNGCHVELLFIRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAINTFKDVFYCWNTFVENHERTFK
AMEGHENSVRLSRQLRTLLDLYEVDDLRDAFRTWGR"
148 t
148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 597)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACA
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/organism:"Homo sapiens"
/db_xref="taxon:9606"
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/db_xref."taxon:10029"
/clone="7"
                                                                            Location/Qualifiers
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/product~"AID"
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                                                /translation="MOSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DFGYLRNKNCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTRATLFFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
MARGLHENGVRLLSCHRILLPLEYDDLRDAFRTWGR"
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Sciurognathi; Muridae;
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/db_xref="G1:22297272"
                                                                                                                                               Score 569;
                                                                                                                                                             Pred. No.
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AF529847.1 GI:22297281
             /product="AID
                                                                                                                                                             100.08;
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Eukaryota; Metazoa;
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                                                                                                                                                           1 Similarity 100.
569; Conservative
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/translation="MOSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRRAPBGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSGTRRILLPLYEVDDLRDAFRTLGL"
163 c 155 g 150 t
                                                                                                                                                                                                                                                                                                                                                                                                596 bp mRNA linear PRI 19-AUG-2002
1 AID (AID) mRNA, partial cds.
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                                                                                                                                                      80 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG 139
                                                                                      TTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA 559
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10461, USA
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                                                                    GCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACC
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; E
Catarrhini; Hominidae;
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B
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99.8%; Pred. No. 9.8e-273;
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/protein_id="AAM95402.1"
/db_xref="GI:22297218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 596
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
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Homo sapiens clone Ramos
AF529815
AF529815.1 GI:22297217
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Mammalia; Eutheria;
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DFGYLRNKNCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSCRRILLPLYEVDDLRDAFRTLGL"
164 c 154 g 150 t
                                                                                  597 bp mRNA linear SYN 19-AUG-2002 clone l transgenic Homo sapiens AID (AID) mRNA,
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                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    " (Mases 1 to 597)
Martin,A. and Scharff,M.D.
Direct Submission (2002) Cell Biology, Albert Einstein College of Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
1 (bases 1 to 597)
1 (bases 1 to 597)
Somartin, A. and Scharff, M.D.
Somartic hypermutation of the AID transgene in B and non-B cells
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="hybridoma pl-5"/transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAM95415.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="1"
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Unpublished
2 (Dases 1 to 596)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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1. 596
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Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Mammalia; Butheria; Primates; Catarrhini; Homini
1 (base 1 to 596)
Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B
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AF529819
AF529819.1 GI:22297225
                                                              Score 545; DB 9;
Pred. No. 9.8e-273;
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/db_xref="G1:22297220"
/db_xref="G1:22297220"
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NLSLRIFTARLYFCEDRRAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
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                           TCCTTTCACTGGACTTTGGTTATCTTCGCAATAACAACGCCTGCCACGTGGAATTGCTC 259
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 596)
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2 AID (AID) mRNA, partial cds.
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/db_xref="taxon:9606"
/clone="Ramos 2"
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Martin, A. and Scharff, M.D.
Direct Submission
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Mammalia; Eutheria; Primates; ... (bases 1 to 596) Martin, A. and Scharff, M.D. Somatic hypermutation of the A
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                                                                                                                           /translation="MDSLLMNRRKFLYOFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DRSTLINKNROCHVELLELRY ISDWDLDGRCK FYTWFTSWSPCYDCARHYADFLEGNP
NLSLR IFTARLY FCEDHKAEPEGLRELHRAGYOLAIWIFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
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6 AID (AID) mRNA,
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Pred. No. 9.8e-273;
0; Mismatches 1;
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                                                                                         /product="AID"
/protein_id="AAM95406.1"
/db_xref="G1:22297226"
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'db_xref="taxon:9606"
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                                                                    /note="integrated
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AF529820
          /clone="Ramos 5'
                                                                              /codon_start=1
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99.8%;
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/gene="AID"
                                 /gene="AID"
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/organisme"Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 8"
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Pred. No. 9
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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99.8%;
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DFGYLRNKNGCHVELLFLRYISDWDPDFRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSCOLRRILLPLYEVDDLRDAFRTLGL"
165 c 155 g 149 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="integrated into Burkitt's lymphoma cell line Ramos"
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
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Somatic hypermutation of the AID transgene in B cells and
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Homo sapiens clone Ramos 7 AID (AID) mRNA, partial cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="GI:22297230"
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                                                                                                                      AF529821.1 GI:22297229
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11 Similarity 99.8%;
595; Conservative
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/translation-"MOSILMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRIRATSFSL
DEGYLRNKNGCHVELLFLRYI SDWDLDPGRCYRVTWFTSWSPCYDGARHVADFLRGNP
NLSLLIFTARLYFCEDRKAEPEGLRRLHRAGVQ1A1MTFKDYFYCWNTFVENHERTFK
MAGGHENSYLSRQLRFLLDLYFEVDDLRDAFRTLGL"
165 g 150 t
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (m.Ju-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin, A. and Scharff, M.D. Somatic hypermutation of the AID transgene in B cells and non-B
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GCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGGGGTGCAAATAGCCATCATGACC
                         TTCAAAGATTATTTTACTGCTGGAATACTTTTTGTAGAAAACCATGAAAGAACTTTTCAAA
                                                                                                             GCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCCAGACAGCTTCGGCGCATCCTT
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Homo sapiens clone Ramos 8 AlD (AlD) mRNA, partial cds.
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Catarrhini; Hominidae;
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. 9.8e-273;
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Il (bases I to 596)
Martin, A. and Scharff, M.D.
              Length 596;
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              Score 545; DB 9; Pred. No. 9.8e-273;
                                          0; Mismatches
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1. .>596
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NLSLRIFTARLYFCEDRRAEPEGLRRLHRAGYQIAIMTFKDYFYCWNTFVENHBRTFR
AWBGLHENSVRLSRQLRRILLPLYFVDDLRDAFRIGL"
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10 AID (AID) mRNA, partial cds.
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Catarrhini; Hominidae; Homo.
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, US 10. 596
Location/Qualifiers
1. 596
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/clone="Ramos 10"
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Mammalia, Eutheria, Primates,
1 (bases 1 to 596)
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/gene="AID"
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AWEGLHENSVRLSRQLRRILLPLYFVDDLRDAFTLGL"
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                                                                        College (10461, U)
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L Unpublished
L Unpublished
L Cases I to 596)
RS Martin, A. and Scharff, M.D.
S Direct Submission
NAL Submitted (17-JUL-2002) Cell Biology, Albert Einstein Coll
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 1047
Location/Qualifiers
Location/Qualifiers
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 AID transgene
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Pred. No. 9.8e-273;
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  Somatic hypermutation
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                                                                            /protein_id="aam95412.1"
/protein_id="aam95412.1"
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/brotein_id="groteingen"
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLAKIFTARLYFCEDRKAEPBGLRRLHRAGYQIAIMTFKDYFYCWNTFVENHERTFK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
Martin, A. and Scharff, M.D.
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                                         /note="integrated into Burkitt's lymphoma cell line
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(AID) mRNA, partial
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Pred. No. 9.8e-273;
0; Mismatches 1;
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                                                       /codon_start=1
                                                                   /product="AID"
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99.8%;
     /gene="AID"
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/gene="AID"
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nes 595; Conservative
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NWEGLHENSYRLSRGFRTLLDLYYFVDDLRDAFRTLGL"
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Sciurognathi, Muridae; Murinae; Mus
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
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Mammalia; Eutheria; Rode
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Martin,A. and Scharff,M.
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/db_xref="G1:22297250"
/translation="MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
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Murinae; Mus
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Sciurognathi; Muridae;
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/db_xref="taxon:9606"
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Mammalla; Eutheria; Rodentia; Sci
1 (bases 1 to 596)
Martin, A. and Scharff,M.D.
Somatic hypermutation of the AII
Unpublished
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LOCUS

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360

619

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/translation="MDSLLMNRRKFLYQFKNVRWAKGRRETYVCYVVKRRDSATSFSL
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NLSLHIFTALFYCEDRKAREPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENGVRLSCHRILLPLYEVDDLRDAFRTLGL"
163 c 156 g 150 t
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                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                             Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
                                                                                                                     cells
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                                                                                                                      transgene
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Pred. No. 9.8e-273;
0; Mismatches 1;
                                                                                                                                                                                                                                                              /cell_type="hybridoma P1-5"
                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAM95422.1"
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                                                                                                                     AID
                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="8"
                                                          Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                               /organism="Homo sapie
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1. .>596
                                                                                                                     of the
                                                                                 wases 1 to 596)
Martin, A. and Scharff, M.D.
Somatic hypermutation of the
Unpublished
                                                                                                                                           2 (bases 1 to 596)
Martin, A. and Scharff, M.D.
                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                      GI:22297257
                                                                                                                                                                                                                                                                                                                                                                                    /product="AID"
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ORIGIN
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AUTHORS
TITLE
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AUTHORS
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             ACCESSION
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KEYWORDS
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRILGL"
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Pred. No. 9.8e-273;
0; Mismatches 1;
                                            /cell_type="hybridoma P1-5"
                                                                                                                                                                                                                                                150
                                                                                                                                                                         /protein_id="AAM95420.1"
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1. 596
∕organism="Mus musculus"
                                                                                 sapiens"
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                                                                                         /db_xref="taxon:9606"
1. .>596
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                                                                               /organism="Homo
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                                                                                                                                                               /product="AID
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99.8%;
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                                                                                                                  /gene-"AID"
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/gene="AID"
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NLSLRIFTARLYFCEDRKAETEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
163 c 155 g 150 t
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
1 .395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells
                                                                                      ATGGACAGCCTCTTGATGAACCGGAGGAAGTTCTTACCAATTCAAAAATGTCCGCTGG
                                                                                                                                                                              TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGG
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                                                                                                                                                                                                                                                                                                TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
                                                                                                                            GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTGAAGAGGCGTGACAGTGCTACA
                                                                                                                                                                    TCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC
                                                                                                                                                                                                          TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG
                                                                                                                                                                                                                                                                                                                            GCTGAGCCCGAGGGGCTGCGGCGCGCGCGCGGGGTGCAAATAGCCATCATGACC
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No. 9.8e-273;
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transgenic P
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 595)
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Martin, A. and Scharff, M.D.
Somatic hypermutation of the
                                                 Score
                                                         Pred.
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Cricetulus griseus clone 1 transgenic Homo sapiens AID (AID) mRNA, complete cds.
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DEGYLRNKOGHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLKGNP
NLSLIFTARLYFCEDRRAEDFGLRRLHRAGVQIAIMTFKDYFYCWNIFVENHERTFK
AWEGHBENSYRLSSQURRILLDLYFVDDLRDAFRTLGL
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Pred. No. 3.3e-272;
0; Mismatches 1;
                                /cell_type="hybridoma Pl-5"
/transgenic
                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                            /protein_id="AAM95421.1"
/db_xref="GI:22297256"
                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .>595
/db_xref="taxon:10090"
/clone="7"
                                                                                                                                                                                                                                                                                                                                154 g
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larity 99.8%;
Conservative (
                                                                                                                                        /gene="AID"
1. .>595
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/translation-"mosllmnrrklyqeknvrmakgrretylgyvkrkidsatsesl
Degylrnkngchvellflry sdwdldpgrcyrvtwftswspcydgrhydflrgnp
NLSLRIFTARLyfcEddrkaepeglrrlhragvqjaimtfkdyfygwnt fvenhertfr
Maeglhensvrlsrqlyfyrddlragvgjaimtfkdyfygwnt fvenhertfr
164 c 165 g 118 t
                                                                                                                                                                                                                                                                  597 bp mRNA linear SYN 19-AUG-2002
3 transgenic Homo sapiens AID (AID) mRNA,
                                                GCTGAGCCCGAGGGGCTGCGGCGCCTGCACCGCGCGGGGGTGCAAATAGCCATCATGACC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 ATGCACAGCCTCTTGATGAACCGGAGGAGTTTCTTTACCAATTCAAAATGTCGGCTGG 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 597)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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                                                                                           560 GCCTGGGAAGGCTGCATGAAAATTCAGTTCGTCTCCAGACAGCTTCGGGGALGCLT
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Somatic hypermutation of the AID transgene in B cells
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Pred. No. 1.6e-267;
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/organtsm."Cricetulus griseus"
/db_xref:"taxon:10029"
/clone."3"
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/db_xrefo"G1:22297274"
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Cricetulus griseus clone
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99.8%;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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1 (bases 1 to 597)
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTIKDYFYCWNTFVENHERTFK
NWEGLHENSVRLSCORRILLPLYEVDDLRDAFRTWGR"
164 c 157 g 147 t
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                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae;
                                                                                                                                                                               Unpublished

2 (bases 1 to 597)

Martin,A and Scharff,M.D.

Martin,A and Scharff,M.D.

Martin,A and Scharff,M.D.

Martin,Companies Scharff,M.D.

Location/Qualifiers

1. .597

/organism="Cricetulus griseus"

/db_xrefe="taxon:10029"

/cell_line="CHO"
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Pred. No. 1.6e-267;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .597
                                                                                                                                                       the AID
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                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                       Somatic hypermutation of
                                                                                                                       1 (bases 1 to 597)
Martin, A. and Scharff, M.
              AF529841.1 GI:22297269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                    /transgenic
1. .597
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ilarity 99.8%;
Conservative
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                                                           Cricetulus griseus
Eukaryota; Metazoa;
                                             Chinese hamster
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/protein_id="AAM95431.1"

ACA_xxef="01:22297276"

//translation="MDSLLMRRKELYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NUSLKIFTARLYFCEDRKAEPEGLRRLHRAGYQIAINTFKDYFYCWNTFVENHERTFK
NUSLKIFTARLYFCEDRKAEPEGLRRLHRAGYQIAINTFKDYFYCWNTFVENHERTFK
AMEGLHENSVRLSRQLRRLLDFYYEVDDLRDAFRTWGR"

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Sciurognathi;
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Pred. No. 1.6e-267;
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the
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/product="AID"
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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/db_xref="taxon:9606"
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/clone="4"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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REFERENCE

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SYN 19-AUG-2002
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DFGYLRNKNGCHVELLFLRYISDWGLDPGRCYRVTWFTSWSPCYDCARHYADFLRGNP
NLSLRIFTARLYFCEDRRAEPEGLRRLHRAGVOIAIMTFKDYFYCWNTFVENHERFFK
AWEGHHENSVRLLSOLRRILLPLYEVDDLRDAFRTWGR"
164 0 188 9 148 L
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Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
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Sclurognathi; Muridae;
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Pred. No. 1.6e-267;
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/protein_id="AAM95435.1"
/db_xrefe="GI:22297284"
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/db_xref-"taxon:9606"
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Martin, A. and Scharff, M.D.
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Mammalia; Eutheria;
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AWEGLHENGVRLSCHRILLPLYEVDDLRDAFRTWGR"
163 c 157 g 149 t
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Pred. No. 1.6e-267;
                                                                          Location/Qualifiers
1. 597
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/cell_line="CHO"
2 (bases 1 to 597)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology,
Medicine, 1300 Morris Park Ave. Chanir
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1. 597
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6 o o o	QY Db	oy Db Oy	Qy Db	Qy Db	Db Qy Db	RESULT 34 AF529850 LOCUS DEFINITION	ACCESTON VERSTON KEYWORDS SOURCE ORGANISM REFERENCE	AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOU
380 AACCCCAACTCAGGATCTTCACCGCGCCCTTACTTCTGTGAGGACCGCAAG 439 111111111111111111111111111111111111	GCCTGGGAAGGCTGCATGAAATTCAGTTCGTCTCTCTCCAGACAGCT 	5 4 2	AF529849 597 bp mRNA linear SYN 19-AUG-2002 ON Cricetulus griseus clone 9 transgenic Homo sapiens AID (AID) mRNA, Complete cds. NAF529849.1 GI:22297285	Chi Chi Euk Mam Cri	IE 1 (bases 1 to 597) S Martin,A. and Scharff,M.D. Concail hypermutation of the AID transgene in B cells and non-B cells L Unpublished P 2 (bases 1 to 597)	Martin, A. Direct Su Submitted Medicine,	9		DEGLERANGE TRANSPORTED TO THE TRANSPORTED TO THE TRANSPORTED TO THE TRANSPORTED THE TRANSPORTE
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AWEGLHBROYRLDFRILLPLYFUDLRDAFRTWGR"
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Martin, A. and Scharff, M.D.
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-210-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
Mammalia; Butheria; Rodentia; Schurognathi; Muridac; Cricetinac;
Cricetulus.
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Pred. No. 1.6e-267;
0; Mismatches 1;
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                                            Martin, A. and Scharff, M.D. Somatic hypermutation of the
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Pred, No. 1.6e-267;
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/translation="MOSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
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AID (AID) MRNA,
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Sciurognathi; Muridae; Cricetinae;
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
                 TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCCGACATGTGGCCGACTTTCTGCGAGGG
                                                                                                                          AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG
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Cricetulus griseus clone 13 transgenic Homo sapiens
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Somatic hypermutation of the AID transgene in
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/db_xref="taxon:10029"
/clone="13"
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/db_xref="GI:22297294"
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Mammalia; Eutheria; Rodentia;
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AF529853
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Abarstal at ion="MOSLLMNRKFLYOFKNVRWAKGRRETYLCYVVKRRDSATSFSL
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NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGYVOIAIMTFKDYFYCWNTFVENHERTFK
AMEGLHENSVRLSRCLAFLUFEVDDLRDAFRTWGR"
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, Nx 10461, USA
                                                                                                                                                                                                                                                                                         Craniata, Vertebrata, Euteleostomi
Sciurognathi, Muridae, Cricetinae,
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GCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCCAGACAGCTTCGGCGCATCCTT
                ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
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Pred. No. 1.6e-267;
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Acganism="Cricetulus gr/db_xref="taxon:10029"
/clone="12"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Martin, A. and Scharff, M.D.
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∕organism⇒"Homo
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/product="AID"
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/protein_idc"AAM95441.1"
/db_xrefc"GI:22297296"
 1. .597
/organism."Cricetulus g
/db_xref."taxon:10029"
/clone."14"
/cell_line."CHO"
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/db_xref⇔"taxon:9606"
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Sciurognathi; Muridae; Cricetinae;
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Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
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                                                                                                                                                                                                           TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG
                                                                                                                                                                                                                                                   TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCCGACTTTCTGCGAGGG
                                                                                                                                                                                                                                                                                            AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG
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AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTWGR"
164 c 156 g 148 t
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                                        Score 535; DB 12;
Pred. No. 1.6e-267;
                                                             0; Mismatches
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                                       19.0%;
99.8%;
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Eukaryota, Metazoa, (
Mammalia, Eutheria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 597)
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chinese hamster
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AF529854
                                                  of Similarity 585; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                        Query Match
Best Local S
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AUTHORS
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AF529854
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/translation-"MDSLLMNRRKFLYOFKNVRWAKGRRETYL-YVVKRRDSATSFSL
DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPWYDCARHVADFLKGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVOIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLLSOLRRILLPLYFUDDLRDAFRTWGR"
163 c 158 g 148 t
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                                                                                                                                                                                                                                                                                                                     259
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                                                                                                                                         Score 535; DB 12;
Pred. No. 1.6e-267;
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Mus musculus clone 13 transgenic Homo sapiens AID (AID) mRNA, complete cds.
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KRUGGHVELLFLXISDWDLDPGRCYRVTWFTSWSPCYDCARHYADFLKGNPNLSLRIF
TARLYFCEDRKAESEGLRLHRAGYQIAIWFFXDYFYCWNTFVENHERTFKAWEGLHE
NSVRLSRQLRRILLEYEVDDLRDAFRLGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 CCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGGCCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTTTTGCCC 625
                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 577)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-B cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 ACCGGAGGAAGTTTCTTTACCAATTCAAAATGTCCGCTGGGCTAAGGGTCGGCGTGAGA
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Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B and Unpublished
                                                                                                                                                                       999
                                                                                                                                                                                      CTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="hybridoma P1-5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAM95427.1"
/db_xref="GI:22297268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            AF529840.1 GI:22297267
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/gene="AID"
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                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                  RESULT 40
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/db_xref="G1:22297288"

/translation="SLLMMRRELYOFKNVRWAKGRCETYLCYVVKRRDSATSFSLDF

/translation="SLDMDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNL

SLRIFTARLYFCEDBRAEPEGLRRLHRAGYOLAIMFTKDYFYCWNTFVENHERTFKAW

EGLHENSVRLSRQLRRILLPLYEVDDLRDAFFTWGR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGAACCCC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACCTCAGTCTGAGGATCTTCACCGCGCCCTCTACTTCTGTGAGGACCGCAAGGCTGAG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 AGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCTACATCTCGGACTGGGACCTAGACCCTGGCGCCTGCTACCGCGTCACCTGGTTCACC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCC 300
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                                                                                            Euteleostomi;
                                                                                                                                                                                                                2 (Cases 1 to 591)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
                                                                                            Craniata; Vertebrata; Euteleostomi
Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                       non-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 529; DB 12;
Pred. No. 2.2e-264;
                                                                                                                                                                                                                                                                                                                       /organism="Cricetulus griseus"
/db_xref="taxon:10029"
/clone="15"
/cell_line="CHO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="AID"
/codon_start=1
/product="AID"
                              AF529855.1 GI:22297297
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99.8%;
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<1. .591
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1. .591
                                                                           Cricetulus griseus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                         Cricetulus.
1 (bases 1 to 591)
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                                                           Chinese hamster.
complete cds.
AF529855
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                             VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AUTHORS
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JOURNAL
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                                                                                                                                                            TCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             596 bp mRNA linear PRI 19-AUG-2002 ^3 AID (AID) mRNA, partial {\rm cds.}
                                                                                                                                                                                                              AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCCCTCTACTTCTGTGAGGACCGCAAG 439
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Martin.A. and Scharff.M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
1. .596
                                                                                          80 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
                                                                                                         TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGG
                                                                                                                                                                                                                                                                                                                   GCTGAGCCCGAGGGGTGCGGCGGCTGCACCGCGGGGGTGCAAATAGCCATGATGACC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 566)
Martin,A, and Scharff,M.D.
                                                                        0;
                                               Length 596
                                                                      Indels
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                                          Score 516; DB 9;
Pred. No. 1.3e-257;
                                                                   0; Mismatches
     151
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/db_xrefe"taxon:9606"
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      5
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     154
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AF529817
AF529817.1 G1:22297221
                                         ich
11 Similarity 99.8%;
566; Conservative
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    163
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Best Local 9
Matches 566
                                         Match
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TITLE
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/fprocedi__id="AAMS4054.1"
/fd_xref="G1:22297224"
/fdranslation="MOSLIAMRRKELYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DFGYLRNKNGGHVELFLRYISDMDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDHKAEPEGLRRHHRAGVQIAIMTFKDYFYCWNTFVENHERTFR
AWEGHHENSVRLSRQLRRILLPLYEVDDL"
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                                                                                                                                                                                                                                                                                                 480
                                                                                                                                                                                                                                                                                                                  AAAAITCAGITCGICTCTCCAGACAGCTTCGGCGCATCCTTTTGCCCCTGIAIGAGGITG 638
                                                                                                                                                                                                                                                                                                                                /note="integrated into Burkitt's lymphoma cell line Ramos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              596 bp mRNA linear PRI 19-AUG-200
4 truncated AID (AID) mRNA, complete cds
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B cells and non-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases I to 596)
Martin, A. and Scharff,M.D.
Direct Submission
Submitted (17-UUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
                                                                                                      GTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGG
                                                                  ACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCT
                                                                                                                                                           GGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGC
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 4"
1. .596
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AF529818
AF529818.1 GI:22297223
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1. 570
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TITLE

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/translation="MOSLLMNRRKFLVQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLFYCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
WHEGLHBNGVRLSDCLRHILLPLYEVDDLRDAFRTLGL"
164 c 153 g 150 t
                                                                                                  College of 10461, USA
                                      cells
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 Murinae;
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                                                                                                 Biology, Albert Einstein
ve. Chanin 404, Bronx, NY
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17.5%; Score 494; DB 12;
Best Local Similarity 99.7%; Pred, No. 3.9e-246;
Matches 594; Conservative 0; Mismatches 2;
                                                                                                                                                                                      /cell_type="hybridoma Pl-5"
/transgenic
                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="5"
                                                                                                                                                                                                                        /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                             /protein_id="AAM95419.1"
/db_xref="GI:22297252"
                                    AID
                                                                                   Direct Submission
Submitted (17-UL-2002) Cell Bio
Medicine, 1300 Morris Park Ave.
Location/Qualifiers
 Rodentia;
                                    the
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             1 (bases 1 to 596)
Martin,A. and Scharff,M.D
Somatic hypermutation of
                                                            2 (bases 1 to 596)
Martin,A. and Scharff,M.
                                                                                                                                                                                                                                                                                                        /codon_start=1
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 Eutheria;
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                                               Unpublished
 Mammalia;
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                                                                                                                        /translation="MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DFGYLRNKNCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADILRGNP
NLSLRIFTRARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDDFYCWNTFVENHERTFK
AMSCLHETAVLLSFQLRRILLEYVDDLRDAFRTLGL"
164 c 156 g 148 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 3.9e-246;
); Mismatches 2;
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                                                                                                /protein_id="AAM95404.1"
/db_xref="G1:22297222"
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Mus musculus clone 5 transgenic
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                                               /gene="AID"
/note="integrated
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                                                                        /codon_start=1
                                                                                     /product="AID"
/clone "Ramos
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99.78;
                      /gene="AID"
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AF529838 596 bp mRNA linear SYN 19-AUG-2002
Mus musculus clone ll transgenic Homo sapiens AID (AID) mKNA,
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163 c 154 9 151 t
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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostoml:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinac: Mus.
1 (bases 1 to 596)
Martin.A. and Scharff.M.D.
Somatic hypermutation of the AID transgene in B and non-H cells
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
    380 AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACGGCAAG
                                                                                                                              GCTGAGCCCGAGGGCCTGCGGCGGCTGCACCGCGCGGGTGCAAATAGCCATCATGACC
                                                                                                                                                                                           TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAA
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Pred. No. 3.9e-246;
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/db_xref:"taxon:10090"
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DFGYLRNNNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAINTFKDYFYCWNTFVENHERTFK
MWEGHHENSVRLSCPRRILLPLYFVDDLRDAFFTLGL"
164 c 153 g 152 t
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10461, USA
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Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B and non-B cells
GCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCACATCCTT
                                   675
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                              TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTG
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Martin,A. and Scharff.M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
Location/Qualifiers
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Pred. No. 3.9e-246;
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/organism="Mus musculus"
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/clone="9"
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/codon_start=1
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LRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDR
KAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLR
RIILPLYEVDDLRDAFRTWGR"
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sequence.
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Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 1.7e-242;
ive 0; Mismatches 0;
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from 2,
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1 (bases 1 to 203250)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
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Homo sapiens BAC clone RP11-83M8
AC007240
             /organism="Homo sapiens"
/db_xref="taxon:9606"
<1. .547
                                                                                                                  /protein_id="AAM95443.1"
/db_xref="G1:22297300"
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Mammalia; Eutheria; Primates;
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                                                                            /gene="AID"
/codon_start=2
                                                                                                       /product="AID"
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                                                    /gene="AID"
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USA
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Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers
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/organism="Cricetulus griseus"
/db_xref="taxon:10029"
/clone="16"
/cell_line="CHO"
/transgenic
  Mismatches
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Rodentia;
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Martin, A. and Scharff, M.D.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Martin,A. and Scharr
  Conservative
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/rpt_family:"MER1_type"
14291. 14620
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'note-"match to EST AA830410 (NID:92903509) or66q10.s1"
                                                                                                                                                                                                                                                                                                                                                                                        'rpt_family="purine-rich"
3778, .13898
                                                                              /rpt_family."MER1_type"
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600. .7910
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911. .8022
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475. .10063
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10526, .10805
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4933. .15196
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(530, .1825
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/clone_lib="RPC1-11"
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16763 .17061
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6100. .6233
/rpt_family~"Alu"
6277. .6395
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10815.
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2855. .2946
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4131. .4414
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1750. .4843
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801. Anon
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12687. .12749
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3972, 1407
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365. 5743
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5751. .6905
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4908. .14932
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5208. .15278
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15496. .15806
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15739. .15806
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17665. .17796
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0501, 10505
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1308. .11598
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Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jul 1, 1999 this sequence version replaced gi:4572726.

Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                              Direct Submission
Submitted (07-APR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                          Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as Compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (Ol-JUL-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                         Cloud, J., Kalicki, J. and Laplant, Y.
The sequence of Homo sapiens BAC clone RPI1-83M8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: H_NH0083M08
Genome Res. 8 (11), 1097-1108 (1998)
99063792
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NEIGHBORING SEQUENCE INFORMATION:
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                                                                         (bases 1 to 203250)
                                                                                                                                                              (bases 1 to 203250)
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Waterston, R.H.
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                                                                                                                                                                                Waterston, R.H.
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                                                                                                                                       Unpublished
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Lustect (27-AUG-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 18540)

Burkngalter, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Chagalter, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Cfand, P., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Janes, C., Landers, T., Lehcozky, J., Leytoek, K., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacCan, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., MacCan, C., Marghy, T., Maylor, J., Melanga, Y., Murphy, T., Naylor, J., Melanga, Y., Murphy, T., Naylor, J., Melanga, Y., Murphy, T., Naylor, J., Melanga, T., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riebeck, M., Silley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stanger-Thommn, N., Stodjanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, P., Willen, Y., Wyman, D., Ye, W.J., Young, G., Lainoun, J., Zainoun, J., Rober, L., Zimmer, A. and Zody, M., Direct, Submission, M., Willer, R., A., Mander, J., Rober, J., Wyman, J., Newers, M., Laine, J., Mander, J., Wyman, J., Newers, M., L., Zimmer, A. and Zody, M., Chander, J., Waller, M., Waller, A., Walle
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Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
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Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
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Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
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Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
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Direct Submission.
                       Boukhgalter, B. Taron, A., Birkett, G., Campoplano, A., Casile, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grahm, L., Grand Pierre, N., Hagos, B., Haeford, A., Horton, L., Illav, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonal, P., Marquis, M., McCarthy, M., McEwan, P., McKernan, K., McDheeters, R., Malquis, M., McCarthy, M., McEwan, P., McKernan, K., Molrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Young, G., Zainoun, J., Kalmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-APR-2002) Whitehead Institute/MIT Center for Genome
      Boquslavkiy, L.,
      Barna, N., Bastien, V., Beda, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC079329 156540 bp DNA linear PRI 20-APR-2002 10mo sapiens chromosome 11, clone RP11-265D17, complete sequence.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1970 GCCGTGGTAGCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo Sapiens chromosome 11, clone RP11-265D17 Unpublished
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Pred. No. 2.1e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="L1"
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Matches 86; Conservative
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SOURCE
ORGANISM
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Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: L10912
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1951. .2104
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    156540
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11570. .11783
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                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              /rpt_family="MIR"
complement(2247.
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/rpt_family="MIR"
8798. .8826
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HOMO Sapiens chromosome 11 clone RP11-133112 map 11, WOKKING DRAFT
SCOURNCE, 8 unordered pieces.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beda, F., Boquslavkiy, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 187836)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 11, clone RP11-133112
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                                                                                                                                                                                                                                                                                                                                                         /rpt_family."MIR3"
complement(22497, .22689)
/rpt_family."MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family."LlPA5"
complement(27157. .27230)
/rpt_family."L2"
27536. .2741
                                                                                                                                   /rpt_family-"MIR3"
7731. .17457
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20274. . 20323
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                                                 /rpt_family~"NIR"
complement(15793. 15857)
/rpt_family~"L2"
16085. 16320
                                                                                                                                                                                                                              rpt_family="MIR3" .19027)
/rpt_family~"AluJo"
complement(15075. .15285)
/rpt_family~"MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                             complement(22767. .23110) /rpt_family~"L2"
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AC023634.3 GI:13357436
HTG, HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens.
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35844. .27056
                                                                                                                                                                                      rpt_family…"(TG)n"
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complement(16384.
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complement(18894.
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complement(27626.
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1013. .21198
                                              complement (15300.
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Best Local Similarity
Matches 79; Conserv
                  repeat_region
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            DeArellano, K., Dewark, K., Dodge, S., Domino, M., Doyle, M.,
DeArellano, K., Dewark, K., Dodge, S., Domino, M., Doyle, M.,
Fenestor, J., Ferreira, P., FitzHugh, M., Forrest, C., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gayette, M., Graham, L.,
Grand-Pierre, M., Grant, G., Horson, R., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Landers, T., Largocque, K., Lehczky, J., Levine, R.,
Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
McDwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Connoll, P., O'Nell, D., Olivar, T. M.,
Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A.,
Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Mu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-FEB-2000) Whitehead Institute/MIT Center for Genome Submitted (16-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2001 Lhis sequence version replaced gi:7767803.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 133_1_12

Sequencing vector: M1: M7815; 56% of reads
Sequencing vector: M1: M7815; 56% of reads
Sequencing vector: Plasmid; n/a: 44% of reads
Sequencing vector: Plasmid; n/a: 44% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 18746 bases at least 040
Consensus quality: 184176 bases at least 040
Consensus quality: 184176 bases at least 020
Insert size: 174000; agarose-fp
Insert size: 174000; agarose-fp
Ouality coverage: 13.0 in 020 bases; agarose-fp
Ouality coverage: 12.1 in 020.

* NOTE: This is a "vorking draft' sequence record is
arbitrary. Gaps between the contigs are represented as
* In to thou and their order in this sequence record is
* In sect will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.
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33787 33886: gap of 100 bp
33887 35099: contig of 1213 bp in length
35200 35199: gap of 100 bp
35200 35514: contig of 1315 bp in length
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36615 37990: contig of 1376 bp in length
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/db_xref="taxon:9606"
/chromosome="11"
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35200 365
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COMMENT

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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (bases I to 41511)
Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W.,
Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S.,
Phan, H., Velasco, M., Garnes, J., Danganan, L., Poundstone, P.,
Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C.,
Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S.,
Lucas, S., Burce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A.,
and Carrano, A.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-APR-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from q centromere to telomere. Cosmid R33496 overlaps cosmid F19987 to the right (by 2.447 kb) and cosmid F25173 to the right. Additional chr 19 map and sequence information may be obtained at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACO04603 41511 bp DNA linear PRI 23-APR-1998
Homo sapiens chromosome 19, cosmid R33496, complete sequence.
ACO04603
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Location/Qualifiers
/clone="RP11-133112"
/clone_lib="RPCI-11 Human Male BAC"
1. .33786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.8%; Score 79; DB 2; L
100.0%; Pred. No. 9.2e-30;
iive 0; Mismatches 0;
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51537 a 44861 c 42761 g 47977 t
                                                                                                              vector_side:left"
3887. .3509
3887. .3509
/note="assembly_fragment"
55200. .36514
/note="assembly_fragment"
3615. .37990
/note="assembly_fragment"
38091. .39599
/note="assembly_fragment"
39700. .41135
                                                                                                                                                                                                                                                                                                                                                                                       41236. .43376
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/note="assembly_fragment
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                                                                                                 clone_end:SP6
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Matches 79; Conservative
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complement(2953). .29623)

/rpt_family-"MER65_internal"
29819. .29969

/rpt_family-"MER5B"

complement(3095). .30994)

/note-"Exon, pregnancy-specific beta-1-glycoprotein 5-like
pseudogene. DPs similarity to (M32635) pregnancy-specific
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24950. 24985
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22812. .23005
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complement(26233. .26594)
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complement(26739. .26502)
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20076. .20439
/rpc_family.~MER50.
complement(20469. .20524)
/rpc_family.~(TA)n.
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complement(32142. .32243)
/rpt_family."MIR"
                            /rpt_family<"Aluy"
(9890, 19024
     complement(18583. .19157)
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32862. 32986
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33029. 35071
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/rpt_family "L1"
32546. 32860
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//note="Cosmid library constructed at LLNL from flow-sorted chromosomes from hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome."
//rpt_family="L1"
//rpt_family="L1"
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.1956. .12076
.1886. .12076
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1. 41511
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9090. 9194
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/rpt_family="FLAM_A"
9878. .10178
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complement(10336. .10493)
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7rpt_rails1

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complement(6387. .5343)

/rpt_family="(AAAA)n"

complement(6365. .6650)

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12969. 13742
/rpt_family="LIMB3"
13743. 14041
14061. 14108
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934. .2630 / rpt_family="L1"
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Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mosten, M., Newtson, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Oragunye, N., Notedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L. L., Ouiles, M., Ren, Y., Rives, M., Rojubokan, I., Rolle, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Yazekk, A., Tabor, P., Tamerisa, A., Tamerisa, R., Tang, H., Tansey, J., Tawerisa, R., Tamerisa, A., Tamerisa, R., Wang, C., Wang, S., Warde, Moore, S., Warren, R., Washington, C., Watlington, S., Walliams, G., Williams, G., Williams, G., Williams, G., Williams, G., Williams, G., Walliams, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, 717 7030, USA on Apr 28, 2002 this sequence version replaced gi:16117994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (11-CCT-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
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Chemistry: Dye-terminator Big Dye: 63% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 117633 bases at least 040
Consensus quality: 148059 bases at least 030
Consensus quality: 148159 bases at least 030
Estimated insert size: 141518; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
Center: project Information
Center project name: HGGG
Center clone name: RP11-502H22
Center clone name: RP11-502H22
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Worley, K.C.
Direct Submission
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                                                                                                                                                complement(36632. .36910)
/note="Exon, pregnancy-specific beta-1-glycoprotein 5-like pseudogene. DPS similarity to (M32635) pregnancy-specific beta-1-glycoprotein 5 [Homo sapiens] (residues 322. .414);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Exon, pregnancy-specific beta-1-glycoprotein 5-like pseudogene. DPS similarity to (M32635) pregnancy-specific beta-1-glycoprotein 5 [Homo sapiens] (residues 415. 499); 91% identity."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                        complement(37853, .37911)
/rpt_family="LiMB1"
37924, .38055
/rpt_family="LiMB1"
38056, .38218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(38485, .38798)
/rpt_family="L1"
complement(38984, .39238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="MER46"
      complement(35975.
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HTG; HTGS_PHASE1.
Homo sapiens.
Homo sapiens
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Teques.15. Clone-eques. Essanger.30.10x
On Jan 11, 1999 this sequence version replaced g1:3927952.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations. Where differences are found these are annotated as variations. State of the overlapping clone, as we submit sequences with a note of the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

In may be shorter because we only sequence overlapping sections once, or longer because we only sequence overlapping sections. The true left end of clone 41018 (AL031732) is at 105499 in this neighbouring submissions.

The true left end of clone 41018 (AL031732) is at 105499 in this sequence. This sequence has been finished according to sequence problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Aln). Where the sequence is ambiguous, there is an annotation using the This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 http://www.sanger.ac.uk/HGP/Chri and Sanger Centre Chromosome 1 http://www.sanger.ac.uk/HGP/Chri and Sanger Centre Chromosome 1 http://www.sanger.ac.uk/HGP/Chri and Sanger Centre de Jong. For further Cancer Institute by the group of Pieter de Jong. For further Cancer Institute by the group of Pieter de Jong. For further Cancer Institute by the group of Pieter de Jong. For further Cancer Institute of Decision and Decision and Decision Sanger.
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Covilla,G.
Direct Submission
                                                                                                                                                                                                                                                  Submitted (28-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clonerequests: clonerequest@sanger.ac.uk
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notes"LIM4 repeat: matches 2652. .2803 of constnsus"
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/note...AluJb repeat: matches 1. .302 of consensus.

2787. .2864

/note...MIR_repeat: matches 124. .204 of consensus.
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note-"AluSx repeat: matches 1. .294 of consensus"

649. .4697
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More--Alusx repeat: matches 3. 295 of conscinsus"
5547. 5578
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hote-"MIR repeat: matches 5. .219 of consensus"
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                                                                              ca repeat polymorphism; D1S2728
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/db_xref~"taxon:9606"
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/clone="RP5-864118"
/clone_lib-"RPCI-5"
808. .998
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/db_xref="taxon:9606"
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'544. .7926
'note="LIMB8 repeat: matches 5786. .6173 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLT1A2 repeat: matches 27. .374 of consensus"
27833. .27889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ### Another Manual Repeat: matches 5. .305 of consensus" 18042. .18164

18042. .18164

18062. .18988

18905. .18988

7note="WIR repeat: matches 25. .249 of consensus" 1802. .20026

7note="WIR repeat: matches 1. .464 of consensus" 1802. .20589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // Anote="Mir repeat: matches 203. .262 of consensus" 17300. .17424 // Anote="Mir repeat: matches 57. .184 of consensus" 17695. .1741 // Anote="L2 repeat: matches 2702. .2750 of consensus" 17742. .18041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Alux repeat: matches 1. .311 of consensus" 24655. .24728
/note="L2 repeat: matches 2340. .2418 of consensus" 24667. .24941
/note="L2 repeat: matches 2673. .2746 of consensus" 26308. .26548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="WIR repeat: matches 91. .228 of consensus"
22106. .22297
/note="L2 repeat: matches 2340. .2522 of consensus"
22269. .22478
                                                                                                                                                                                                                                                                                                                                                                                                                                        note="L2 repeat: matches 2639. .2707 of consensus"
[5180. .15335
                                                                                                                                                                                                                                                                 .2748 of consensus"
                                                                                                                                                                                                                                                                                                                   12772. .12926
"note="MER5A repeat: matches 9. .188 of consensus"
13655. .13766
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[6311, .16375
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27324. .27372
                                  /note="Alus repeat: matches 1. .304 of consensus" 3502. .8642
                                                                                                                                                                                                                                                                                              note-"MIR repeat: matches 24. .140 of consensus" 2772. .12926
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fnote="MIR repeat: matches 24. .135 of consensus"
13946. .14088
fnote="MIR repeat: matches 90. .259 of consensus"
15024. .15089
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(6823. .27105
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21341. 21485
                                                                  8502. 8642

//ote=milk repeat: matches 74...

9934. 10017

/note="MIR repeat: matches 49...]

10945. 111392

/note="MSTB repeat: matches 1...

11531. 11586
                                                                                                                                                                                                                         /note="MIR repeat: matches 91.
12186. .12369
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15511. .15805
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                               Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 109538)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                         Direct Submission
Submitted (27-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut creek, CA 94598, USA
On Feb 27, 2002 this sequence version replaced gi:15290413.
Draft Sequence Produced by DOE Joint Genome Institute
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Catarrhini; Hominidae; Homo.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 109538)
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                                                                    DOE Joint Genome Institute and Stanford Human Genome Center,
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HOMO Sapiens PAC clone RP4-764012 from 7, complete sequence.
AC006476
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence:
Estimated Total Number of Errors is 0.1.
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The sequence of Homo sapiens PAC clone RP4-764012
Unpublished
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Sulston, J.E. and Waterston, R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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DOE Joint Genome Institute.
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. Werberson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov, or see http://genome.wustl.edu/usv
                                                                                                                                                                                                                                                                                                                                                                                               Missouri 63108, USA
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                                                                         Direct Submission
Submitted (29-MAY-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was continued by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A tandem repeat, extending from base position 67681 to 71791, has been sorted to best possible assembly. Restriction digest information with bambi, hindili, and ecory suggests this region is missing approximately 1400 base pairs of sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The clone sequenced to the left is RP5-1058P19. Actual start of this clone is at base position 1 of RP4-764012; actual end is at 112804 of RP4-764012.
                                                                                                                                                                                                                                                                                                                                                                                               University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On May 29, 1999 this sequence version replaced g1:4337287.
                                                                                                                                                                                                                                                                                                                 Direct Submission Submitted (30-SEP-2000) Department of Genetics, Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
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The clone may be obtained either from Genome Systems, (http://www.genomesystems.com) or Research Genetics, (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: H_DJ0764012
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NEIGHBORING SEQUENCE INFORMATION:
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/db_xref:"taxon:9606"
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4 (bases 1 to 112804)
Waterston, R.H.
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101773 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAG 101714
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AY052369.1 GI:16303629
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Muneer,S., Kamibayashi,C. and Minna,J.D.

Direct Submission
Submitsed (24 MG-2001) Hamon Center for Therapeutic Oncology,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd, Dallas, TX 75390, USA
Location/Qualifiers
1. 121028
//Organism="Homo sapiens"
//db_xref="taxon:9606"
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Muneer, S., Ramalingam, V., Wyatt, R., Schultz, R.A., Minna, J.D. and Kamibayashi, C.
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7.7pt_family="L1"
35690. 37077
7.0ct="C9G island (%GC=63.0, o/e=0.90, #CpGs=106)"
37890. 40107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 112804;
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Best Local Similarity 100.0%; Pred. No. 1e-28;
Matches 77; Conservative 0; Mismatches 0; Indels
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2285. 33146
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AUTHORS
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                                                                                                                                     note-"match to EST AI568539 (NID:g4531913) tn40e08.xl"
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9202. 9330
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10090. 10212
/rpt_family="L"
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.575. .1615
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Mammalia; Eutheria Prinates; Catarrhin; Hominidae; Hamo.

1 (bases 1 to 126295)

Muzny, D.M., Addms.C., Adio-Oduola, B., Alt-Osman, F.R., Allen, C., Adio-Oduola, B., Alt-Osman, F.R., Allen, C., Adio-Oduola, B., Alt-Osman, F.R., Allen, C., Barbooks, S.L., Amaratuqe, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Burberia, J., Benton, J., Brieva, M., Brown, E., Brown, M., Bryant, N. C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N. C., Carrer, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., Duvid, R., Davila, M.L., Dayar, Carroll, L., Dagar, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gao, J., Garcia, A., Garner, T., Garza, N., Glil, K., Garza, N., Gao, J., Garcia, A., Garner, T., Garza, N., Garcia, A., Garner, T., Garza, N., Gall, Harris, C., Harris, C., Harris, C., Harris, C., Hart, M., Havlash, P., Hawes, M., Hollows, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hullyk, S., Hume, J.,
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Homo sapiens 3 BAC RP11-435F17 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AC079944
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GSIINGFRLPLKEEHKIFLLKVLLPLHKVKSLSVYHPQLAYCVQFLEKDSTLTEPVY
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RALYYWNNEYIMSLISDNAAKILPIMFPSLYRNSKTHWNKTIHGLIYNALKLFMEMNQ
KLFDDCTQQFKAEKLKEKLKMKEREEBAWVKIENLAKANPQAQKDPKKDRPLALRKSEL
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Submitted (21-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 21, 2002 this sequence version replaced gi:21465331.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

gc-help@bcm.tmc.edu

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < le-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

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QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot
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                                                                                                                   source
                                                                                                  FEATURES
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* NOTE: Estimated insert size may differ from sequence length

* See http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* Consists of 10 contigs. The true order of the pleases

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                           Direct Submission
Submitted (11-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 4, 2000 this sequence version replaced g1:9929481.
                                                                                                                                                                                                                                                                                                 Chemistry: Dye-primer Bodipy: 80% of reads
Chemistry: Dye-terminator Biq Dye: 20% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 1566% bases at least 040
Consensus quality: 156644 bases at least 020
Estimated insert size: 15239; sum-of-contigs estimation
Ouality coverage: 0x in 020 bases; agarose-fp estimation
Quality coverage: 5x in 020 bases; sum-of-contiqs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51941: contig of 51941 bp in length 65204: gap of unknown length 85871: contig of 33830 bp in length 85871: gap of unknown length 99094: contig of 13123 bp in length 99194: gap of unknown length 109291: contig of 10097 bp in length 10939: gap of unknown length 118498: contig of 9877 bp in length 118598: gap of unknown length 127575: contig of 8977 bp in length 127575: contig of 8977 bp in length 135234: contig of 7559 bp in length 135344: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908 others
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150682: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.7%; Score 77; DB 2;
ilarity 100.0%; Pred. No. 1e-28;
Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29406 c 27663 g 48296 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142541: contig of 7207
142641: gap of unknown
                                                                                                                                                                                                                                                 Center clone name: RP11-22G4
----- Summary Statistics
Sequencing vector: M13; L08821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism∵"Homo sapiens'
/db_xref∵"taxon:9606"
                                                                                                                                                                                                                                Center project name: HCAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone-"RP11-22G4"
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   (bases 1 to 154968)
                                                                                                                                                           Center code: BCM
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Best Local Similarity
Matches 77; Conserv
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52042
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ORIGIN
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.7%; Score 77; DB 9; Length 126;
100.0%; Pred. No. 1e-28;
ive 0; Mismatches 0; Indels
            /rpt_family="Alusc"
15787. .15813
/rpt_family="(TAA)n"
complement(15848. .16146)
/rpt_family="Alusx"
16268. .16323
                                                                                         /rpt_family="AT_rich"
complement(16839. 16778)
/rpt_family="L2"
17560. 1750.
                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="MER58B"
23728. .23752
                                                                                                                                                                                                                                                                                                                                 /rpt_family="MER94"
complement(22567. .22692)
/rpt_family="L2"
                                                                                                                                                                                       /rpt_family="AT_rich" complement(19788. .20005)
                                                                                                                                                                                                                            /rpt_family="L2"
complement(20100. .20384)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                      /rpt_family="AluSx" 32446. .22574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
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21645. .21
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Best Local Similarity 100.0
Tranes 77: Conservative
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
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RESULT 57 AC078928

g ô ACCESSION

KEYWORDS SOURCE

REFERENCE AUTHORS

q à

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4208

4208

57969 58068: gap of

57969 7743: contig of 15675 or

73744 73843: gap of 100 bp

* 73844 87132: contig of 13289 bp in length

87133 87232: gap of 100 bp

87233 105996: contig of 18764 bp in length

7233 105996: contig of 100 bp
                                                                                                                                                                                                                                                                                                                                                               10597 106096: gap of 100 bp 106097 127200: contig of 21104 bp in length 127201 127300: gap of 100 bp 127301 162958: contig of 35658 bp in length.
1646 1688: contig of 43 bp in length 1689 1788: gap of 100 bp 1789 13851: contig of 12063 bp in length 1352 13951: gap of 100 bp 13952 27920: contig of 13969 bp in length
                                                                 51: gap of 100 bp
27920: contig of 13969 bp in length
                                                                                                                                                         p of 100 bp contig of 15888 bp in length
                                                                                                                                      in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-11 Human Male BAC"
                                                                                                             ap of 100 bp contig of 13960 bp
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100.0%; Pred. No. 10.
... 0; Mismatches
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31972 c 32404 g 47242 t
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13952. .27920

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28021. .41980

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42081. .57968

/note="assembly_fragment"

58069. .73743

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87233. .105996
/note="assembly_fragment"
106097. .127200
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27301. .162958
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/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-318C12"
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J: gap of
57968: 7
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28021 41980; cont
41981 42080; gap of
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VERSION
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Lisfaye, S., Tiltell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Lisct Submission

Mar 26, 2000 this sequence version replaced gi:6630602.

All repeats were identified using Repeatmasker:
                                                                                                                               ACULIU22 162958 bp DNA linear HTG 26-MAR-2000 HOMO sapiens clone RP11-318C12, WORKING DRAFT SEQUENCE, 11 UNDERGRED PIECES.
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center clone name: 318_C_12
Sequencing vector: M13, M7815, 100% of reads
Sequencing vector: M13, M7815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 154951 bases at least Q40
Consensus quality: 159946 bases at least Q30
Consensus quality: 161045 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 168001 agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 4.9 in Q20 bases; agarose-fp Quality coverage: 5.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 \\ 1545 contig of 1545 bp in length 1546 1645; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 162958)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-318C12
U (bases 1 to 162958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------- Project Information
Center project name: L1785
                                                                                                                                                                                                                                        AC011022.4 GI:7329290
HTG; HTGS_PHASE1; HTGS_DRAFT:
Homo sapiens.
                         126137 GAGGTGGAGGTTGCAGT 126153
2039 GAGGTGGAGGTTGCAGT 2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                          AC011022
                                                                                                                                                                       DEFINITION
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AUTHORS
TITLE
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REFERENCE
AUTHORS
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JOURNAL
                                                                                                             RESULT 58
AC011022
                                                                                                                                                                                                                      ACCESSION
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KEYWORDS
SOURCE
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1979 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAG 2038
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                                                                                                                                                                                                                                                   Homo sapiens chromosome 16 clone RP11-44F14, complete sequence. AC007342.5 GI:15808502
                                                                              Gaps
                                                                            .;
0
                                          Score 77; DB 2; Length 162958;
Pred. No. 1e-28;
0; Mismatches 0; Indels 0
1001 others
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AL391866.8 G1:13561275
HTG; HTGS_PHASE1; HTGS_CANCELLED
                                                                                                                                           (bases 1 to 181183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: SC
                                                                             Homo sapiens
                                                                                                                                                                    Mclay, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1979 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAG 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (bases 1 to 17777)

DOE Joint Genome Institute.

DOE Joint Genome Institute.

DOE Joint Genome Institute.

Submitted (29-SEP-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Sep 29, 2001 this sequence version replaced gi:14589412.

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than lerror in 10,000 bp.
                                                                                                                                                                                                       Druce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltble, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L. Direct Submission Submission Submitted (21-APR-1999) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NW 87555, USA
                                                                     Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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100.0%; Pred. No. 1e-28;
tive 0; Mismatches 0; Indels 0
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37201 c 36594 g 50744 t
                                                                Eukaryota, Metazoa, Chordata, Cran
Mammalia, Eutheria, Primates, Cata
I (bases 1 to 17777)
DOE Joint Genome Institute,
Sequencing of Human Chromosome 16
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/db_xref="taxon:9606"
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1. 177777
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                        Homo sapiens.
                                                 Homo sapiens
                                                                                                                                                                                      Unpublished
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Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
on or before May 15, 2001 this sequence version replaced
gi:8901286, gi:10186833.
Direct Sequence Produced by Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7915; 46% of reads
Sequencing vector: M13; M7915; 46% of reads
Sequencing vector: plasmid: L08752; 53% of reads
Chemistry: Dyo-terminator Big Dyo; 53% of reads
Chemistry: Dyo-terminator Big Dyo; 53% of reads
Consensus quality: 179412 bases at least Q40
Consensus quality: 179718 bases at least Q40
Consensus quality: 180265 bases at least Q20
Insert size: 180883; sum-of-contigs
Insert size: 180883; l.2% error; agarose-fp
Quality coverage: 7,89x in Q20 bases; sum-of-contigs Oudlity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 104210 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23472: contig of 23472 bp in length 23473 23572: app of 100 bp 60332 60331: contig of 36759 bp in length 60332 60431: gap of 100 bp 60432 164641: contig of 104210 bp in length 16432 16741: gap of 104210 bp in length 164742 181183: contig of 16442 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                   http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism∵"Homo sapiens'
/db_xref∵"taxon:9606"
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/clonec."RP11-315J13"
/clone_lib="RPCI-111.2"
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1. .181183
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188863 bp DNA linear PRI 04-NOV-2000 Homo sapiens chromosome 16 clone RP11-466N18, complete sequence. AC007345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There, D. Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Campbell, C., Tesmert, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1979 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAG
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76531 179019: contig of unknown length 79020 179119: gap of unknown length 79020 179119: gap of unknown length 1966 182065: gap of unknown length 1866 186431: contig of 4366 bp in length 1.0 Coation/Qualifiers 4366 bp in length 1.1.186431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               848 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.7%; Score 77; DB 2; Length 186 Best Local Similarity 100.0%; Pred. No. 1e-28; Matches 77; Conservative 0; Mismatches 0; Indels
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/note="assembly_name:Contig235"
176531. 179019
/note="assembly_name:Contig231"
179120. 181965
/note="assembly_name:Contig231"
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126025. .128493
./note="assembly_name:Contig233"
128594. .156515
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156616. .170011
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/note="assembly_name:Contig236
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124826. .125924
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a 41798 c 41896 g 53062 t
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Organism="Homo sapiens"
/db_xref="texon:9606"
/chromosome="10"
/clone="RP11-10E13"
/clone="RP11-1DE13"
1 124725
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1 (bases 1 to 188863)
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Homo sapiens
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179120
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                                                                                                                               Submitted (28-JAN-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA On Mar 21, 2001 this sequence version replaced gi:9929643.
                                                                                                           2038
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186431)
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                                                                                                         1979 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAATCGCTTGAACCCAG
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Phrap; version 990315
Consensus quality: 395389 bases at least Q40
Consensus quality: 405067 bases at least Q30
Consensus quality: 410525 bases at least Q30
Insert size: 185631; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                        AC022281.3 GI:13399348
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN;
HTGS_CANCELLED.
HOMO Saptiens.
HOMO saptiens
                                                                                                                                                                                                                                                                                                                                         ACO22281 186431 bp DNA linear HTG 24 Homo sapiens chromosome 10 clone RP11-10E13, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
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Center code: GTC
Web site: http://www.genomecorp.com/
                          Length 181183;
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                                                                 0; Indels
                        DB 2;
1e-28;
                        2.7%; Score 77; DB
100.0%; Pred. No. 1e-
live 0; Mismatches
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                                                                                                                                                                                          2039 GAGGTGGAGGTTGCAGT 2055
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Smith, D.R.
                                         Local Similarity 100.
nes 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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AC022281
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Gaps ö 0;

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PRI 04-SEP-2001

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Genoscope.

Direct Submission
Submitted (04-SEP-2001) Genoscope - Centre National de Sequencaqe :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@qenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 194871)
1 (bases 1 to 194871)
1 (bases) To Cattolico, L., Barbe, V., Pelletler, E., Artiquenuve, F., Cruy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissenbach, J.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The following BAC sequence is oriented from the T7 to the SP6 end. Obstream BAC (overlapping the T7 end) : C-2017C7 Downstream BAC (overlapping the SP6 end) : R-114H15 (AC ALL14221)
                                                                                                                                                                                                                                                                                                                                                                                                      CNSOlDRV 194871 bp DNA linear PKI 04-SEP-20C Human chromosome 14 DNA sequence BAC R-1017G21 of library RPCI-11 from chromosome 14 of Homo saplens (Human), complete sequence.
                                                                                      1979 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAG

    - Web : www.genoscope.cns.fr)
    On Sep 6, 2001 this sequence version replaced g1:14571656.

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Quality coverage: 9.00x in 020 bases; sum-of-contiqs
                                   Indels
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                             0
     Pred. No. 1e-28;
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                             0; Mismatches
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/db_xrefe"taxon:9606"
/chromosomee:"14"
/clonee"R-1017G21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: SeqRef@genoscope.cns.fr
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1. .194871
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Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-MAY-2002) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriégec.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) On Aug 9, 2002 this sequence version replaced gi:21624263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRI 10-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP005264 192539 bp DNA linear PRI 10-AUG-2007
Homo sapiens genomic DNA, chromosome 18 clone:RP11-64C12, complete
                                                           Theory of the control of the control
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Genome Institute, Los Alamos National Laboratory, MS M888, Los
Alamos, NM 87545, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.7%; Score 77; DB 9; Length 188863;
100.0%; Pred. No. 1e-28;
Live 0; Mismatches 0; Indels 0.
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36866 c 36556 g 58384 t
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51833 a 45020 c 43248 g 52438
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/db_xref~"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                            1. .188863
/organism="Homo sapiens"
/db_xrefo"taxon:9606"
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Center: Joint Genome Institute
Center Code: JGI
Web Site: http://www.jgi.doe.gov
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 225432)

Chi, H.-C., Saunders, E.H., Buckingham, J.M., Ricke, D.O., Munk, C.C.,
Lobb, R.R., Ueng, S. T.-J., Mundt, M.O., White, P.S., Tatum, O.L.,

Riethman, H.C. and Moyzis, R.K.

DNA Sequence Analysis of the Terminal 226 kb of Human Chromosome 7q

Unpublished

C. (Dases 1 to 225432)

E. (Dases 2 to 225432)

E. (Dases 2 to 225432)

E. (Dases 3 to 225432)

E. (Dases 3 to 225432)

E. (Dases 4 to 225432)

E. (Dases 1 to 225432)

E. (Dases 1 to 225432)

E. (Dases 2 to 225432)

E. (Dases 3 to 225432)

E. (Dases 3 to 225432)

E. (Dases 3 to 225432)

E. (Dases 4 to 225432)

E. (Dases 4 to 225432)

E. (Dases 5 to 225432)

E. (Dases 6 to 225432)

E. (Dases 7 to 225432)

E. (Dases 8 to 225432)

E. (Dases 8 to 225432)

E. (Dases 9 to 225432)

E. (Dases 9 to 225432)

E. (Dases 1 to 225432)

E. (Dases 2 to 225432)

E. (Dases
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19550. .19636
/note="80% identity"
/db_xref="80% identity"
19655. .19824
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8171. .8421
/note="GRAIL 2 good exon ; ORF; frame 0"
8929. .9106
12304. .12466
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901. .1496
/note="HSAL000641"
/rpt_family="Alu"
complement(2341. .2376)
/note="GRAIL 2 good exon ; ORF; frame 0"
2513. .2800
/note="M32220"
                                                                                                     linear
                                                                                                AF027390 225432 bp DNA 1
Homo sapiens 7q telomere, complete sequence.
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/rpt_family="Alu"
complement(12621, 12766)
/note="97% identity -- U66083"
complement(12792, 14659)
/rpt_family="L1"
complement(14751, 14845)
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/note="80% identity -- Z77249"
19840. .19998
/note="83% identity"
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20128. .20260
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complement(12460. .12687)
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2659. 2897
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4101. 4283
/note="HSAL006653"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .225432
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/chromosome="7"
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                                                                                                                                                                                                                                                  Homo sapiens
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/note="matching EMBL:N46343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identified using the e-PCR software (G. Schuler)" 161688. .161880 .7note="matching EMBL:T86293 RHD:RR17951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identified using the e-PCR software (G. Schuler)" 178326. .178431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dbSTS:STS22994
Identified using the e-PCR software (G. Schuler)"
49542 a 46484 c 46814 g 52031 t
                                                                                                                     dbSTS:STS3660
Identified using the e-PCR software (G. Schuler)"
53216. .53395
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Identified using the e-PCR software (G. Schuler)"
178303. 178552
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178392. .178577
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Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                       dbSTS:STS21713
Identified using the e-PCR software (G. Schuler)"
76990. .77117
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100.0%; Pred. No. 1e-28;
Live 0; Mismatches (
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RHdb:RH92864
                    92484. 92604
/note="matching EMBL:H97017
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RHdb:RH8632
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RHdb:RH53557
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clone_lib="RPCI-11"
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dbSTS:STS38832
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Matches 77; Conserv
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.37580)

misc_feature

/note-"81% identity -- Z77249"

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124031 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAG 123972
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complement(58350. .58466)
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62145. .62245
/note="GRAIL 2 good exon ; ORF; frame 2"
complement(65881 .64744)
/rpt_family="Tigger!"
/rpt_family="Tig
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/note--"GRAIL 2 good exon; ORF; frame 1"

complement (48123. .48196)

/note--"MALR00106"

/rpt_family--"MLT-e"

complement (49320. .49497)

/note--"GRAIL 2 excellent exon; ORF; frame 2"

complement (4934. .50215)

/note--"GRAIL 2 good exon; ORF; frame 2"

complement(5133. .51901)

/note--"GRAIL 2 good exon; ORF; frame 2"

complement(51240. .552500)
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100.0%; Pred. No. 1e-28;
ive 0; Mismatches 0; Indels 0
                                                                                                               ... complement(41427. .41642)
/rpt_family"MLT2B2"
complement(42308. .42622)
/rpt_family""MLT2B2"
/ rpt_family""Tigger2"
43821. .44600
/ note""GRAIL 2 good exon ; ORF; frame 2"
/ note""GRAIL 2 good exon ; ORF; frame 2"
/ note""GRAIL 2 good exon ; ORF; frame 1"
/ note""GRAIL 2 good exon ; ORF; frame 1"
/ note""GRAIL 2 good exon ; ORF; frame 1"
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complement(46801. .47121)
/note="HSAL005507"
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     /note."84% identity"
/db_xref."dbEST:T62489"
complement(37828. .38086)
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complement(47511.
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Best Local Similarity 100.
Matches 77; Conservative
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/db_xref="GI:3004859"
/translation="MRTLLPPALLTCWLLAPVNSIHPECRFHLEIQEEETKCAELLRS
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orecursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //octe="99% identity -- L40764"
Complement(join(<31908. .32006,34182. .34234))
/gene="VIP2R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(<31907. .32006,34182. .34394))
/gene="VIP2R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement[27361. .27462)
/note="GRALL 2 excellent exon; ORF; frame 2"
/note="GRALL 2 good exon; ORF; frame 2"
/note="GRALL 2 good exon; ORF; frame 2"
/note="Analysis"
21027. .21097
/note="GRAIL 2 excellent exon ; ORF; frame 2"
complement(24077. .24350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="TARI"
35000..35058
35000..35058
complement(35325..35445)
/rpt_family="MRR42"
/rpt_family="MRR42"
/rote-"HSAL004342"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MER33"
31815. .31991
Ance="GRAIL 2 good exon; ORF; frame 1"
complement(<31907. .34394)
/gene="VIP2R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /youte="100% identity -- L40764"
complement(34200. 34394)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 //note-"100% identity -- 259087"
complement(34182. .34232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="92% identity -- L36566"
4432. .34694
                                                                                                                                                                                   /rpt_family="Alu"
24633. 24901
/rpt_family="Alu"
complement(24992. .25278)
/note="Z73359"
                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="THE1"
complement(25777. .25901)
/note="MALR00322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="HSAL004729"
rpt_familu=".
                                                                                                       /rpt_family="Alu"
complement(24301. .24492)
/note="HSAL000410"
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complement(37248. .37455)
/note="MER4_00001"
/rpt_family="MER4"
                                                                                                                                                                                                                                                                                                                   /rpt_family="Alu"
complement(25515. .25599)
/note="MALR00365"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MSTc"
complement(26808. .27050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor"
complement(31907. .32006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(33411. .33597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="Alu"
complement(27009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="X66298"
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DEFINITION

AC011933

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

JOURNAL JOURNAL AUTHORS

AUTHORS TITLE

REFERENCE

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S. (Dascal Lo. 1997.25)
Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Mandtha, Meldrim, J., Meneus, L., Minhova, T., Malega, V., Murphy, T., Naylor, J., Maneus, L., Minhova, T., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schubback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zalnoun, J., Sembel I., Vimmer, B., Stange-Thoman, R., Young, G., Zalnoun, J., Sembel I., Vimmer, B., Stange-Thoman, N., Stojanovic, N., Vonne, I., Vo, A., Vimmer, B., Wu, X., Wyman, D., Young, G., Zalnoun, J., Sembel I., Vimmer, B., Stange-Thoman, W., Vonne, V., Stanger, B., Wu, X., Wyman, D., Young, G., Zalnoun, J., Sembel I., Vo, A., Vimmer, B., Stange-Thoman, W., Vonne, V., Vonne,
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27812 CAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGG 27871
                                                                                                                                                                                                                                                                                                                                                                                                     AC100787 199725 bp DNA linear HTG 20-AUG-2002 Homo sapiens chromosome 17 clone CTD-2589J4 map 17, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On AUg 20, 2002 this sequence version replaced gi:17048157. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 199725)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC100787.2 GI:22325312
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone CTD-2589J4
Unpublished
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                                                                                                                                   27872 AGGTGGAGGTTGCAGT 27887
                                                                                         2040 AGGTGGAGGTTGCAGT 2055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
                                                                                                                                                                                                                                                                                                                                                                AC100787/c
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KEYWORDS
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                                          HTG 31-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (16-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Dec 31, 2001 this sequence version replaced gi:15451715.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                     153300 bp DNA linear HTG 31-DEC-2
11-16C1, *** SEQUENCING IN PROGRESS ***, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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                                                                                                                                                                                                                   AC011933.13 GI:18001668
HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-16C1
Unpublished
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                                                                               Homo sapiens clone RP11-16C1, ordered pieces.
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Best Local Similarity
Matches 76; Conserv
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TITLE JOURNAL

COMMENT

Source

FEATURES

BASE COUNT

ORIGIN

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JOURNAL
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome, clone RP11-30023
                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Homo sapiens clone RP11-30023, LOW-PASS SEQUENCE SAMPLING.
ACU24328
                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length 199725;
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                         Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center: project Information
Center project name: 120503
Center clone name: 2589_J_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                     39561 39660: gap of 100 bp 39661 199725: contig of 160065 bp in length. Location/Qualifiers
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100.0%; Pred. No. 3.4e-28;
Live 0; Mismatches 0;
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50529 c 51605 g 47969 t
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/db_xref="taxon:9606"
/chromosome="17"
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HTG; HTGS_PHASE0.
                                                                                           Center code: WIBR
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Matches 76; Conservative
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Homo sapiens
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AC024328
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VERSION
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TITLE
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REFERENCE
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Meneus, L., Mihova, T., Miranda, C., Mienga, V., Merrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Clivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Schauer, S., Schauer, S., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tircell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                   Genome
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., McKernan, K., McPheeters, R., Moldrim, J.,
                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                              Submitted (28-FBB-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using Repeatmasker: Smit, A.F. A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/Repeatmasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This record contains 84 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          659 758: gap of 100 bp 1759 1471: contig of 713 bp in length 1472 1571: gap of 100 bp 16572 2278: contig of 777 bp in length 1279 2378: gap of 100 bp 100 bp 1379 3055: contig of 677 bp in length
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14894: contig of 705 bp in length
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contig of 688 bp in
of 100 bp
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10189: contig of 706 bp in
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10190 10289: gap or
10290 10972: contig of 683 bp in
10973 11072: gap of
100 bp
11744: contig of 672 bp in
11744: contig of 672 bp in
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3155: gap of 100 bp
3155: gap of 100 bp
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contig of 694 bp
of 100 bp
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of 100 bp
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contig of 697 bp
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13302: contig of 695 bp
02: gap of 100 bp
14089: contig of 687 bp
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5398: con
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6192: con
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3165 33264; gap of 100 bp 13265 33938; contig of 674 bp in length 13939 34038; gap of 100 bp 14039 34751; contig of 713 bp in length 14652 34851; gap of 100 bp 15562 3561; gap of 100 bp 100
15703: contig of 709 bp in length 15703: contig of 709 bp in length 16511: contig of 708 bp in length 6611: gap of 100 bp in length 1784; contig of 673 bp in length 7384; gap of 100 bp in length 18098: contig of 714 bp in length
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20486: contig of 676 bp in length
20586: gap of 100 bp
21266: contig of 680 bp in length
21366: gap of 100 bp
22034: contig of 668 bp in length
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29152: contig of 665 bp in length
2954: contig of 665 bp in length
2954: contig of 692 bp in length
30044: gap of 100 bp
30733: contig of 689 bp in length
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1649 32356: contig of 708 bp in length
1357 32456: gap of 100 bp
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41925 42607: contig of 683 bp in length
4208 427707: gap of 100 bp
42708 4341: contig of 704 bp in length
43412 43511: gap of 100 bp
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 66792)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (28-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Feb 28, 2001 this sequence version replaced gi:9256040.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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58 50657: gap of 100 bp
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41 52240: contig of 700 bp in length
41 52240: gap of 100 bp in length
41 52240: gap of 100 bp in length
41 52332: contig of 692 bp in length
33 53033: gap of 100 bp
53719: contig of 687 bp in length
52 53819: gap of 100 bp
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Pred. No. 3.8e-27;
0; Mismatches 0;
               18 44317.37; Cont.19 100 bp 118 45001; Cont.19 01684 bp 100 2 45101; gap of 100 bp 100 2 45101; gap of 100 bp 100 2 4583; gap of 100 bp 100 47368; cont.19 of 693 bp 100 47368; cont.19 of 693 bp 100 47368; gap of 100 bp 100 bp 100 48249; cont.19 of 601 bp 100 48249; cont.19 of 707 bp 100 50 48249; cont.19 of 707 bp 10
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DOE Joint Genome Institute
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Best Local Similarity 100.0%; P:
Matches 74; Conservative 0;
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AUTHORS
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Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
NO 63108, USA
4 (bases 1 to 118958)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (13-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 118958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases I to 118958)
Sulston, J. E. and Waterston, R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACU92579 118958 bp DNA linear PRI 21-1
Homo sapiens BAC clone RP11-15K19 from 7, complete sequence.
AC092579 AC011922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Feb 13, 2002 this sequence version replaced gi:18425307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center
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0
                                                                                                                                                                                                                            Length 66792;
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Cordum,H., Elliott,G., Spalding,L. and Phillips,A.
The sequence of Homo sapiens BAC clone RP11-15K19
Upublished (2001)
3 (bases 1 to 118958)
Waterston,R.H.
                                                                                                                                                                                                                                                                Indels
Quality: Phrap Quality >=40 99.6% of Sequence;
                                                                                                                                                                                                                        Query Match 2.6%; Score 74; DB 9; Lei
Best Local Similarity 100.0%; Pred. No. 3.8e-27;
Matches 74; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
....... Summary Statistics
Center project name: H_NH0015K19
              Estimated Total Number of Errors is 0.2
Location/Qualifiers
1. 66792
/organism="Homo sapiens"
                                                                                               /db_xref="taxon:9606"
/chromosome="19"
/clone="CTD-3023J11"
16364 a 17164 c 17596 g 15668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                        FEATURES
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosom? 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov.pr. Seed mailto:egreen@nhgri.nih.gov.pr. seed http://qenome.wustl.edu/qsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The clone sequenced to the left is RPI1-419M24, 2000 bp overlap; the clone sequenced to the right is RPI1-745J15. Actual start of this clone is at base position 160861 of RPI1-419M24; actual end is at base position 118958 of RPI1-15K19.
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                  all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phicd quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, H., Frengen, E. Tateno, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to EST AA922972 (NID:93070281) ok77d11.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228. .245 | hotem match to EST W02526 (NID:91274505) 7448c05.rl"
                                                                                                                                                                      This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of AC011922 has been incorporated into AC092579
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.646. .1957
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318. .993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Data from AC092101 was used to finish AC092579
                                                                                                        between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism∵"Homo sapiens"
/db_xref∵"taxon:9606"
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1053. .1499
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1. .118958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family "MaLR"
2271 .3282
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193. .497
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321. .1090
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/note:"match t
3283. .3428
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2920. 2920
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Gaps

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158213 bp DNA linear HTG 26-JUL-2002 Homo sapiens chromosome 8 clone XX-CTB788C1, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                                                                                                                                                                              1982 GGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAG 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 158213)
Reichwald, K., Baumgart, C., Blechschmidt, K., Dette, M., Jahn, N., Lehmann, R., Menzel, U., Polley, A., Schilhabel, M.B., Schudy, A., Siddiqui, R., Taudien, S., Wen, G., Korenberg, J.R., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 158213)
Reichwald, K., Blechschmidt, K., Menzel, U., Baumgart, C., Dette, M.,
Jahn, N., Schilhabel, M., Korenberg, J.R. and Rosenthal, A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrapa assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13; 100% of reads
Sequencing vector: M13; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 146316 bases at least Q40
Consensus quality: 151479 bases at least Q30
Consensus quality: 154827 bases at least Q20
Quality coverage: 5.51 x in Q20 bases; sum-of-contigs
 /note="match to EST AL539603 (NID:g12868971)"
                                                                                                                /note="match to EST BE827799 (NID:g10260177)"
                                                                                                                                                   Length 118958;
             12558. .12697
/hote="match to EST AA358556 (NID:92010873)"
12558. .12697
                                                                        /note="match to EST BE439838 (NID:99439449)" 12558. .12697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF214635.3 GI:14280180
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
HOMO Sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.6%; Score 74; DB 9; L. Best Local Similarity 100.0%; Pred. No. 3.7e-27; Matches 74; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: XX-CTB788C1
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Chromosome 8 genomic sequence
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                     misc_feature
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AUTHORS
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AUTHORS
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AF214635
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KEYWORDS
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                                                                                                                                                                                                                        /rpt_family="Alu"
2248. 5250
/note="match to EST N68717 (NID:g1224878) za20a06.s1"
3376. 5830
/note="match to EST AI492948 (NID:g4393951) qz47a04.x1
                                                                                                                                                                                                                                                                                                   5933. "S. 6286

f. far. family="MaLR"

6328. .6602

/rpt_family="Alu"

6340. .6369

/rote-mach to EST N68717 (NID:91224878) za20a06.s1"

6988. .7281
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1260. .11309
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match to EST BE439838 (NID:99439449)"
11297. .11309
/note="match to EST AA358556 (NID:92010873)"
11341. .11655
/note="match to EST BF237438 (NID:911151356)"
11678. .11750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "note="match to EST B1458323 (NID:g15248979)"
1.280. .11309
"note="match to EST BE827799 (NID:g10260177)"
1.281. .11309
                                                                            /note-"match to EST AW903301 (NID:98067506)"
1086. .4447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L1"
8888. 8115
/note="similar to Homo sapiens EST BI856928
(NID:915997675)"
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12044. .12049
/note="match to EST N55773 (NID:g1198621)"
12129. .12428
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/rpt_family="L1"
10415. 10718
/rpt_family="Alu"
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/rpt_family="MaLR"
3503. .3812
/rpt_family="Alu"
4056
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11830. .12121
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602. .9904
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9905. 1010.
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10192. .10412
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12550. 12697
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213. .9329
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3330. .9601
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Direct Submission

Submitted (33-DEC-2001) Whitehead Institute/MIT Center for Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Birren B., Linton.L., Nusbaum,C., Lander,E., Ali A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,

Chazarc,B., Choepel,Y., Colangelo,M., Campoplano,A., Clanqu,J.,

Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodqe,S.,

Faro,S., Ferreira,P., FitzHudh,W., Gage,D., Galagain,J., Gardyna,S.,

Ginde,S., Gord,S., Goyette,M., Grahm,L., Grand-Pherre,N.,

Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,

Kamat,A., Karatas,A., Lakels,C., LaRocque,K., Landazarcs,R.,

Landers,T., Lehcozky,J., Levine,R., Lindblad-Toh,K., Iliu,G.,

MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,

MacCarthy,M., MecPan,P., McKernan,K., Matdrim,J., Matthews,C.,

Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Nell,D.,

Oliver,J., Petterson,K., Phunkhang,P., Plerre,N., Pollara,V.,

Raymond,C., Retta,R., Rleback,M., Riley,R., Rise,C., Roqov,P.,

Roman,J., Rosetti,M., Roy,A., Santos,R., Schupback,R., Stolanovic,N.,

Strauss,N., Subramanian,A., Talanas,J., Tesfaye,S., Theodorc,J.,

Viel,R., VO,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.,

Direct Submission
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Houkhdalter, B., Choepel. T., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dolias, S., Collymore, S., Faro, S., Faro, S., Farreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Harton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karlas, A., Kells, C., Levine, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Norman, C.H., O'Connor, T., O'Connor, T., Wolhel, D., O'Neil, D., O'Neil, D., O'Liver, J., Retta, R., Plander, W., Plant, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Roqov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauers, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Lainner, A., and Zody, M., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boukhgalter, B. Brown, A., Camarata, J., Campoplano, A., Chanq, J., Chagelly, Characta, J., Campoplano, A., Chanq, J., Colagelly, Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., Farchiano, K., Dewar, K., Diaz, J.S., Dodge, S., Farceira, P., Fitzhugh, W., Cage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Lakocque, K., Landarath, R., Karatas, A., Kalls, C., Lakocque, K., Linu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, J., Marquis, M., McEwan, P., McKernan, K., Medrim, J., Mennus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Well, D., Olluver, J., Petta, R., Phunkhang, P., Pierre, M., Pollura, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rougo, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rougo, P., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Stolanovic, N., Stolanovic, N., Stolanovic, M., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Ve, W.J., Yound, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.
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Research, 320 Charles Street, Cambridge, MA 02141, USA
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
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JOURNAL
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                              NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                         3530: contig of 3530 bp in length 3630; gap of unknown length 5231: contig of 1501 bp in length 5231: gap of unknown length 1345: contig of 8214 bp in length 13545: gap of unknown length 31026: contig of 17481 bp in length 31026: gap of unknown length 51905: contig of 20779 bp in length 52005: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   800 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 43289 bp in length gap of unknown length contig of 3375 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 29561 bp in length
gap of unknown length
contig of 29683 bp in length
gap of unknown length
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone CTC-788C1
Unpublished
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/note="assembly_fragment
clone_end:SP6
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/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="XX-CTB788C1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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158210. .158213
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Best Local Similarity
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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
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129206 CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGAGAATCGCTTGAACCCAGGAGGTGG 129147
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Homo sapiens chromosome 12 clone RP11-414A12, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
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AC068793.19 GI:21431064
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AUTHORS
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Direct Submission
Submitted (27-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 21, 2002 this sequence version replaced gi:20128267. All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasKer.html
                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L21405
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complement(9353. .9430)
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14152. .14451
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14452. .14520
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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.B., Delaney, K.B., Delaney, K.J., Delaney, R.J., Douthwaite, K.J., Delaney, R.J., Dudan-Rocha, S., Durbin, K.J., Bouthwaite, K.J., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Falls, T., Gao, J., Garcia, M., Ganer, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Henrandez, O., Hodgson, A., Hatt, M., Holloway, C., Hanris, C., Harris, K., Huber, J., Hulyk, S., Hume, J., Jackson, L. B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Lui, J., Lui, M., Lui, M., Loulsewid, H., Louzedo, R.J., Lui, M., Lucier, R., Martinez, E., Mawhiney, E., McLeed, M. P., Meador, M., Martinez, E., Mawhiney, E., McLeed, M. P., Meador, M., Martinez, E., Mawhiney, E., McLeed, M. P., Meador, M., Mguyen, N., Nickerson, E., Mwitchell, T., Mohabbat, K., Morgan, M., Morser, M., Neal, D., Newtson, N., Nguyen, N., Nguyen, N., Nguyen, N., Nickerson, E., Shoalker, Payton, B., Peerry, G., Shen, H., Shoshtari, M., Shoon, I., Sondergren, E., Sondake, T., Yapior, T., Telfrod, B., Tamerisa, K., Tang, H., Sutton, M., Sotter, Sondake, T., Yapior, T., Telfrod, B., Tamerisa, K., Tang, Y., Tansey, J., Taylor, C., Walls, M., Wolen, W., Thomas, S., Usuliams, G., Walliams, G., Wallen, S., Warren, R., Washington, C., Walliams, G., Wallen, S., Warren, R., Washington, C., Walliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Warley, R., Wooden, S., Walliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Walliams, G., Walliams, G
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Submitted (18-70W-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA
On Jun 17, 2002 this sequence version replaced gi:20335641.
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* NoTE: This is a "vorking draft" sequence. It currently

* NoTE: This of 8 contigs. The true order of the pieces

* consists of 8 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
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----- Summary Statistics
Sequencing vector: M13;
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Direct Submission
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COMMENT

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manufatis Euromital Findless Catafronni Hominidae: Homo.

Bodota, B. Bouck, J. Bailey, M., Barbaria, J., Blankenburg, K.,

Bodota, B., Bouck, J., Brooks, A., Bulaby, C., Bunac, C.,

Burkett, C., Burrows, J., Carter, M., Ding, Y., Domah-Rashid, N.,

David, R., Delgado, O., Deshaco, D., Ding, Y., Domah-Rashid, N.,

Dugan Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,

Forcum-Tansey, J., Frantz, P., Ganseh, R., Gorrell, J.H., Gorrell, L.L.,

Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hoques, M.,

Jones, W., Kelly, S., Knetiz, S., Kondejewski, N., Kong, Y., Kovar, C.,

Lau, S., Leal, B., Lee, E., Li, Z., Lichtarge, O., Liu, J., Liu, W.,

Logan, O., Lozado, R.J., Lu, J., Lucier, R., Marondel, I., Martin, R.,

Martinez, C., McLeody, M., Morris, S., Nash, S., Miller, A.,

Mourgomery, K.T., Morgan, M., Morris, S., Nash, S., Naison, A.,

Samuel, S., Say, J., Scherer, S., Shap, E., Shen, H., Shim, C., Simon, M.,

Sparks, A., Stamps, A., Sucgang, R., Tabor, P., Taylor, T., Vasquez, L.,

Vinson, R., Vo, O., Wahbah, M., Watlington, S., Weinstock, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC012156 162200 bp DNA linear PRI 12-AUG-2000 Homo sapiens 12p11-37.2-54.4 BAC RP11-433D24 (Rosewell Park Cancer Institute Human Bac Library) complete sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                         as soon as it is available and the accession number will be preserved.
arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                  contig of 5965 bp in length
contig of 6296 bp in length
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gap of unknown length
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Weinstock,I.R., Williamson,A., Worley,K., Wren,J., Wrensford,G.,
Xhang,A.M., Yang,R., Yu,W., Zhou,X., Kucherlapati,R., Nelson,D. and
Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
Submitted (12-AUG-2000) Human Genome Sequencing Center, Department
Submitted (12-AUG-2000) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Mar 31, 2000 this sequence version replaced gi:7211838.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                   Direct Submission
Submitted (21-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases I to 162200)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                            Submitted (31-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 162200)
                                                                                                   Unpublished
2. (bases 1 to 162200)
Worley, K.C.
                                                                            Direct Submission
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

COMMENT

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < le-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERACE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

OUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT------

	162200 156878	0.000360119	53
Summary Statistics	Contig length:	Average error rate (BCM-Phrap estimate):	Number of consensus changing edits:
	Phrap values in estimate:	Fraction of Phrap values less than 40	Number of N's in consensus :

its	Edited+Context	agttact	arceratg(r)rererere ttootatgt(t)tttttt	toctatgit(t)tttttttt	ttttttt(t)gagacag	tttaagaca(g)acagagte tttgagaca(g)agtettge	ggctgattt(c)tttttgtat	atttttag(t)ggagacgcg	tttagtgga(g)acgcggtt accatatta(a)ccadatu	tectaacet(e)ataateegg	ctgacctcg(t)gatccgccc	tecgeceat(e)teggeceee	cgcccatct(c)ggcccccca	acctcttc(t)acacagaca	tacaaa(a)coocaaaace	gagrada (r) ccagacad	ggtacacct(c)ccagacggg	actetggag (g) tgaageaca	ctggaggt(g)aagcaca	ccctaagt(c)cctgtctgc ttttattaa(a)aaagggaag	tttagatgg(t)attttctc	agaattttc(c)accataaac	agctgactt(c)attatgcc	acaaagtac(a)ctcccttca	adytacacte(c)ecteatt adtacacte(c)etteattt	ggtgaacac(c)tgtagtccc	gigaacacc(t)giagiccca	cccagcct(c)taagta	tttt(c)ttccacttc tttaa(g)aaacagag	ceccccaa(g)acacagage caaatatac(a)cttacttaa	gaaaaaat(a)caataaag	gccactgca(c)tgcactcca	ggaggctga(g)gcagccggg	cryayycay(c)cyyyyaycre	agccgg(g)agttcgaga	gcagccggg(a)gttcgagac	cagccggga(g)ttcgagacc	agccgggag(L)tcgagacc	cyyyay ccc y jayaccaycc tototttaa (a)aaaqaaaag	aaagcaaca(a)taaaagaaa	tggāgtgca(a)tggtgtgat	gcaatggtg(t)gatctcggc	tecgeetec(c)aggtteaag	ă č	0 Bases	*	*	*
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Submitted (22-JUN-2000) Production Sequencing Facility, DOE Joint Schome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 167722)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167722)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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Submitted (31-010-2002) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Greek, CA 94598, USA
On Jul 31, 2002 this sequence version replaced gi:15022024.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC073548 167722 bp DNA linear PRI 31-JUL-
HOMO sapiens chromosome 19 clone RP11-43N16, complete sequence.
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Finishing Completed at Stanford Human Genome Center
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quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.7.
NOTE: Forced join 65004.
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100.0%; Pred. No. 3.7e-27;
iive 0; Mismatches 0;
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/rpt_family~"(CA)n"
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/rpt_family="LiMa6"
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1 (Bases I to 16924)

Raul,R.K., Yu,J., Wong,G.K.-S., Magness,C.L., Green,E.D., Green,P. Large-scale MCD Mapping and Sequencing of Human Chromosome 7 Unpublished
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Sequencing vector: M13: 100% of reads
Chemistry: Dye-ptimer Bodipy: 90% of reads
Chemistry: Dye-terminator Big Dye: 10% of reads
Assembly program: Phrap: version 0.990319
Insert size: 169 234; sum-of-contigs
Quality coverage: 11.1X in Q20 bases; sum-of-contigs
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46532 c 43717 g 39144 t
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/db_xref."taxon:9606"
/chromosome."19"
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65004
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4492.00 4478.00 10778.00 10756.00 10111.00 9669.00 3278.00 3209.00 1250.00 1234.00 11366.00 11758.00 1347.00 1339.00 2135.00 2108.00 4059.00 3979.00 8691.00 8644.00 5075.00 4993.00 1997.00 1990.00 1347.00 1331.00 897.00 875.00 2570.00 2445.00 4350.00 4341.00 1103.00 1082.00 2570.00 2276.00	12901.00 12601.00 3635.00 3602.00 11366.00 11207.00 3278.00 3339.00 11685.00 11548.00 10111.00 10101.00 12901.00 13224.00 1410.00 1385.00 13982.00 13668.00 3051.00 3072.00 2819.00 2826.00 5487.00 5487.00 5453.00 19500.00 19348.00 2076.00 2128.00 4140.00 4057.00 1535.00 1554.00 2745.00 2716.00	3063.00 1734.00 	1147.00	897.00 888.00 677.00 688.00 677.00 966.00 995.00	FEATURES Location/Qualifiers source 1. 169234 /organism="Homo sapiens" /db_xref="taxon:9606"	/chromosome="/" /map="7p14-15" /clone="djs1 (RP11-16G1)" /cell_line="Male Blood" /clone_lib="RPC-11 Human Male BAC Library" repeat_region 392. 494	repeat_region / tptamily= mert 1364) /rpt_family="Alu" STS complement (1210, 1237) /standard_name="swSS2626" /note="GenBank Accession Number: G12923" /rote="GenBank Accession Number: G12923"	repeat_region /rpt_family="MLT1" repeat_region /rpt_family="MLT1" repeat_region complement(44894790) /rpt_family="Alu" repeat_region complement(53075594) /rpt_family="Alu" SH76152 /rpt_family="Alu" STS /rpt_family="Alu" complement(69707082) /standard_name="swss1000" /note="GenBank Accession Number: G00158"
This entry has been annotated with sequence quality estimates computed by the phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part Double stranded (DS) coverage: 96.4% Bs or two chemistry coverage: 97.1% Single stranded regions:	alidated on of the predicte ted sequent rately reariable fingerpino signification of signification of signification of signification of signification of sequent secore signification of signific	FP Seq FP Seq FP Seq 2055.00 2061.00 8954.00 8687.00 11080.00 11109.00 5487.00 5270.00 7660.00 4611.00 4562.00	1508.00 13322.00 4399.00 7336.00 11080.00 11183.00 1508.00 13291.00 13322.00 4399.00 4333.00 2193.00 2193.00	1004.00 992.00 4140.00 4094.00 3735.00 3692.00 529.00 503.00 660.00 643.00 614.00 599.00 10358 00 10526.00 3053.00 3100.00 3918.00 3851.00	3819.00 5075.00 5106.00 614.00 593 1645.00 6909.00 6771.00 2570.00 2518 2170.00 1911.00 1874.00 1995.00 1995	3051.00 2974.00 3635.00 3584.00 6199.00 6176.00 14433.00 14779.00 3975.00 3996.00 4913.00 5009.00 1508.00 1475.00 897.00 864.00 2193.00 2184.00	1865.00 1874.00 1410.00 1399.00 12585.00 12586.00 2228.00 2269.00 5716.00 5790.00 1819.00 1821.00 2055.00 2043.00 3306.00 3304.00 709.00 690.00 1347 00 1325.00 3475 00 3843.00 6428.00 6484.00	00 4449.00 897.00 876.00 1944.00 1934 00 3757.00 7648.00 7475.00 3127.00 3138 00 3031.00 3635.00 3611.00 16492.00 16338 00 1676.00 838.00 824.00 2842.00 2741 00 10132.00 3053.00 2987.00 6528.00 6572

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4444 Forest Park Parkway, St. Louis,
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                             1982 GGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCCAGGAG
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                     172816 bp DNA linear PRI 12-JU AC093899 AC068884 AC093899.3 GI:18497265 HTG.
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Submitted (10-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. M 05108, USA
4 (bases 1 to 172816)
Waterston, R. H.
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                                                                                                                        Length 169234;
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Pearman,C., Haakenson,W. and Boyer,E.
The sequence of Homo sapiens BAC clone RP11-724016
Mpublished (2001)
3 (bases 1 to 172816)
Waterston,R.H.
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Contact: sapiens@watson.wustl.edu
                                                                                                                                            3.7e-27;
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                                                                                                                            DB 9;
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                              /rpt_family="Alu"
10137. .10423
/rpt_family="Alu"
complement(7545. .7634)
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                                                                                                                            Score 74;
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Submitted (05-FEB-2002) Genome
University School of Medicine,
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Mammalla; Eutheria; Primates;
1 (bases 1 to 172816)
Sulston,J.E. and Waterston,R.
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Best Local Similarity
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     repeat_region
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AC093899/c
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TITLE
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MEDLINE
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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                    all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by sequence from more than one subclone; and the assembly was contirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEICHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RPI1-724016;
actual end is at base position 172816 of RPI1-724016.
This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of AC068884 has been incorporated into AC093899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/chromosome-"2"
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19. .1140
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1. 172816
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1141. .1437
/rpt_family~"Alu"
1438. .2657
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011 .5263
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8360. .8551
/rpt_family:"L1"
8622. .8718
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7807. .7952
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5285. .5907
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(321, 3642
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4185. .4996
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7103. .7421
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2730. .3320
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/rpt_family…"MIR'

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25920. 26206
/rpt_family="Alu"
26893. 26917
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/rpt_family="(A)n"
9882..10166
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?5030. 25506
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29485, 20502
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.6886. 1716
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29811. .29874
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Siren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bouguslavki, L., Boukhgalter, B., Brown, A., Burkett, G., Captagolo, M., Collins, S., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Deawar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Klein, J., Carlow, C., Hangos, E., Heaford, A., Horton, L., Kaling, J., Lakoque, K., Landarases, R., Landers, T., Lehcotzky, J., Levine, R., Lakoque, K., Landarases, R., McCarthy, M., McBewan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McBewan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McBewan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McBewan, P., McGurk, A., McKernan, K., McDreat, S., McCarthy, M., Stolaner, C., Riley, R., Spencer, B., McCarthy, M., Stolaner, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Subramanian, A., Trigilio, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Stolaner, S., Street, Cambridge, MA 02141, USA

Submitted (09-Mar-2000) Whitehead institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Submitted, Submission

Cock, A., Cocke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fare, Ener, P., Horton, L., Hulme, W., Cillins, S., Collymore, A., Gardyna, S., Ferreira, P., Pitzdera, J., Candpell, Y., Calagae, H., Calagae, H., Horton, L., Hulme, W., Cillins, S., Calagae, J., Horton, L., Mage, M., Horton, M., Machena, R., Mores, R., Menders, T., Menders, T., Menders, M., Matthews
                                                                                                                                                                                                                                                                             AC025518 176355 bp DNA linear PRI 29-JUN-2002
Homo sapiens chromosome 17, clone RPI1-713H12, complete sequence.
AC025518
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 17, clone RP11-713H12
Unpublished
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100.0%; Pred. No. 3.7e-27;
iive 0; Mismatches 0;
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/rpt_family."MIR" .20535)
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21147. .21645
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complement(10889. 10989)

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11195. 11449
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complement(15990, 16001)
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/rpt_family "L2"
complement(21797. 21897)
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complement(22822. 22940)
/rpt_family."MIR3"
complement(23073. 23362)
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complement(13667. .14961)
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913. .8940
                                          complement(5183. .5252)
/rpt_family."HAL1"
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20262. .20301
/rpt_family "(CAT)n"
complement(20318. .20
                                                                                                         rpt_family .. "CT-rich"
                         ′rpt_family…"(TTTC)n"
                                                                                                                                                                                                                                                                                                                                                         "(TTTG)n"
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7060. .17202
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[8788. .18850
                                                                                                                                                    "AluSx"
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7224. .17534
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11755. 12059
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complement(12811.
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18911. .18947
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17609. .18017
                                                                                                                                               /rpt_family…"
6636. .6943
/rpt_family…"
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                                                                                                                                                          L. Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (16355)

E. (Dases I to 176355)

Barran, N. Bastlen, V. Bloom, T. Boguslavkiy, L. Boukhgalter, B. Camarata, J. Chang, J. Chazaro, B., Choepel, Y., Collymore, B., Cook, A., Cook, P., DeArellano, K., Dowar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N. Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Marthews, C., Karatas, A., Kalls, C., Landers, T., Marthews, C., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., MucDily, T., Naylor, J., Ngoy, R., Norbu, C., Norman, C., Norman, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Talamas, J., Tesfâve, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Zimmer, A. and Zody, M., Zemběk, L., Zimmer, A. and Zody, M., Zemběk, L., Zimmer, A. and Zody, M., Direct Submission
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Savery, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vasslilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 0. Jun 2002 this sequence version replaced g1:21427869.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI-11 Human Male BAC"
complement(30..88)
/rpt_family="L3"
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1380. .244i
/rpt_family~"L2"
complement(2781. .2876)
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/db_xref="taxon:9606"
/chromosome=="17"
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/rpt_family="L3"
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/rpt_family="(TAAA)n"
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4449. .4745
/rpt_family="Alusg"
4931. .4987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP11-713H12"
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/rpt_family="L2"
1380. 2444
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                                                                                                    Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 9, 2002 this sequence version replaced gi:13677173.
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                                                                                                                                                                                                                                                                                             PRI 09-JAN-2002
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Louis,
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Submitted (19-APR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                               1982 GGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAG
                                          Gaps
                                                                                                                                                                                                                                                                                 Homo sapiens BAC clone RP11-567N19 from 2, complete sequence. AC016772.9 GI:18098289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (04-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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0
    Length 176355;
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Has sequence of Homo sapiens BAC clone RP11-567N19
Unpublished (2001)
3 (bases 1 to 176932)
Waterston, R.H.
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Query Match 2.6%; Score 74; DB 9; L
Best Local Similarity 100.0%; Pred. No. 3.7e-27;
Matches 74; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 176932)
Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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......... Summary Statistics
Center project name: H_NH0567N19
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7 (bases 1 to 176932)
                                                                                                                                                                               Submitted (07-NOV-2001)
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Waterston, R.H.
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhoo, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE CHOOKING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-401019; the clone sequenced to the right is AC068884. Actual end of this clone is at base position 176932 of RP11-567N19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="similar to Mus musculus EST AA538008 (NID:g2284001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541. .921
/note="similar to Mus musculus EST AA106541 (NID:91657130)
                                                                                                                                                                                all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="similar to Bos taurus EST AV596137 (NID:g9713168)"
                             clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112. 507
'note="match to EST AA918024 (NID:93057914) ol73d08.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="match to EST AA769615 (NID:92820853) ob19906.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. IMO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                      This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST B1976350 (NID:g16350755)"
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/note="similar to Mus musculus EST BI455611
(NID:915246267)"
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/db_xref="taxon:9606"
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note="similar to Mus

NID:910977890)"
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1. 176932
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239. .639
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1550. .1950
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Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 18209)

Birren B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhqalter, B.,

Camardata, J., Chang, J., Chazaro, B., Chopel, Y., Collymore, A.,

Cook, A., Cooke, P., DeArellano, K., Dewar K., Diaz, J.S., Bodqe, S.,

Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,

Gardyna, S., Gord, S., Graham, L., Grand-Plerre, N., Haqos, B.,

Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A.,

Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,

Liu, G., MacLean, C., Macdonald, P., Major, J., Marthows, C., Mcarthy, T., Maylor, J., Nauyen, C., Nicol, R., Norbu, C., Norman, C., Morcathy, M., Waldrin, J., Meneus, L., Mihova, T., Mlenga, V.,

Phunkhang, P., Plerre, N., Raymon, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schuebz, S., Schupback, R., Seaman, S., Severy, P.,

Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zalnoun, J.,

Direct submission
                                                                                        AC026130 182909 bp DNA linear PRI 14-JUL-2002
Homo sapiens chromosome 17, clone RP11-801J18, complete sequence.
AC026130
                                                            1982 GGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATGGCTTGAACCCAGGAG 2041
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 182909)
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Homo sapiens chromosome 17, clone RP11-801J18
Unpublished
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      Mismatches
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Matches 74; Conservative
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SOURCE
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AUTHORS
TITLE
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REFERENCE
AUTHORS
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JOURNAL
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/note="match to EST BI550291 (NID:915437603)"
4489. .4659 /note="similar to Bos taurus EST AV596137 (NID:99713168)"
/note="similar to EST BI976350 (NID:916350755)"
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6370. .6664
6773. .6807
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(NID:91246267)"
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4089. 4101

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(NID:915250402)"

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/note="match to EST AV648795 (NID:99869809)"

/note="match to EST AV648795 (NID:99869809)"
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Anote-"match to EST A1424984 (NID:94270915) tg38h07.x1"
3720. 3833
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4489. .4659
4489. .4659
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Mote-similar to EST B1976350 (NID:g16350755)"

7555 . 7555

Mote-"match to EST B1550291 (NID:g15437603)"
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/note="match to EST BG106656 (NID:912600502)"
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6773. .6805
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NID:915246267)"
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5978. .6366
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3425. .3655
/rpt_family="MIR"
3714. .3942
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1987. .5025
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Chazaror, B., Cheepel, Y., Collymore, A., Camarata, J., Chang, J., Collymore, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Gard, S., Gard, S., Gard, M., Gage, D., Galagan, J., Gard, S., Gard, S., Gard, M., Gard, M., Gange, D., Galagan, J., Lulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Mayon, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rase, C., Rogov, P., Roman, J., Roy, A., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Talamas, J., Vell, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Jul 6, 2002 this sequence version replaced gi:21426269.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
....---- Project Information
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93. .407
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complement(1561. .1784)
/rpt_family="LiMB7"
complement(1789. .2051)
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Y="Alusx"
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/rpt_family="L2"
complement(13603, ...13706)
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Center clone name: 801_J_18
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/note="<30 qual SNGL region" complement(21530, .21538) /note="<30 qual SNGL region" 22759. 23068 23122. 23128 /note="<30 qual SNGL region" 23138. 23151 /note="<30 qual SNGL region" /rpt_famlly="LiMA2" complement(28085..28239) /rpt_famlly="LiME3" /rpt_famlly="LiME3" /rpt_family="AluSp" 36008. .36054 /rpt_family="L3" 36097. .36121 /note="<30 qual SNGL region" complement(21443. .21745) /rpt_family="Aluy" complement(21508. .21516) complement(19092. .19180)
/rpt_family="LJME3"
20169. .20453
/rpt_family="AluJb"
20454. .20497
/rpt_family="(CA)n"
20552. .20576
/rpt_family="(CA)n"
complement(120585. .20813) /rpt_family"LlMC5"
complement(27053...27364)
/rpt_family"AluSq"
complement(27417...27477)
/rpt_family="U7"
.complement(27487...27525)
/rpt_family="LIMA2"
27526...27586
/rpt_family="(TA)n" /rpt_family="Alusq"
complement(32603, 32002)
'rpt family="Alusq" /rpt_family="MER7C" :0200. :3040= /rpt_family="L2" complement(20874. .21062) /rpt_family="L2" complement(21389. .21395) complement(18391. .18472)
/rpt_family="L1ME4A" complement(23462...23640) rpt_family="AluJo/FRAM" 'rpt_family="(TATATG)n" :8831. .28851 /rpt_family="AT_rich" complement(29182. .29 rpt_family="AluSx" 'rpt_family="AluSx" 'rpt_family="AluJo" 10436. .30555 rpt_family="MIR" . rpt_family="Aluy" 8831. .28851 6691. .26909 repeat_region repeat_region

Ouery Match 2.6%; Score 74; DB 9; Length 182909; Best Local Similarity 100.0%; Pred. No. 3.7e-27; Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps

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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1. (bases 1 to 186870)

2. (bases 1 to 186870)

3. (bases 1 to 186870)

Barna, N. Bastien, V. Bloom, T. Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Chopel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, R., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Mathews, C., Norman, C., Naccarthy, M., Meldrin, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., Punkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seanan, S., Severy, D., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, R., Lahmer, A. and Zody, M., Waman, D., Young, G., Zainoun, J., Direct, Shmission
AC116170 186870 bp DNA linear HTG 24-AUG-2002 Homo sapiens chromosome 17 clone RP11-855E10 map 17, WORKING DRAFT SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186870)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP11-855E10
Unpublished
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AC116170.2 GI:22474934
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AC116170
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...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                    Center clope name: 855_E_10

Sequencing vector: Plasmid: n/a; 100% of reads
Sequencing vector: Plasmid: n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 185544 bases at least 040
Consensus quality: 185963 bases at least 020
Insert size: 188000; agarose-fp
Insert size: 188570; aum-of-contigs
Quality coverage: 17.0 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * arbitrary, Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently * consists of 4 contigs. The true order of the piecus * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 186870;
                                                                       16662 16761; gap of 100 bp
16762 42342; contig of 25581 bp in length
42343 42442; gap of 100 bp
44443 114057; contig of 71615 bp in length
114058 114157; gap of 100 bp
114158 166870; contig of 72713 bp in length
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/clone_lib∵"RPC1-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 74; DB 2; L
Pred. No. 3.7e-27;
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40568 c 39916 g 54513 t
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/organism "Homo sapiens"
/db_xref "taxon:9606"
/chromosome "17"
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Best Local Similarity 100.
Matches 74; Conservative
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SOURCE

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PRI 06-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                      Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Consensus quality: 178595 bases at least 040
Consensus quality: 182392 bases at least 030
Consensus quality: 184739 bases at least 020
Estimated insert size: 184304; sum-of-contigs estimation
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of 12900 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 12671 bp in length
unknown length
of 15448 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 35467 bp in length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 10811 bp in length
                                                                                                                 Chemistry: Dye-primer Bodipy: 54% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown length
of 31039 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.6%; Score 74; DB 2; I
100.0%; Pred. No. 3.7e-27;
Live 0; Mismatches 0;
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                             Center clone name: RP11-64L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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contig
gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="3"
                                                                                      Sequencing vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2042 GTGGAGGTTGCAGT 2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 GTGGAGGTTGCAGT 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24676:
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Best Local Similarity 100.0
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                            I (Dasses I to 1879)

Radiany, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C., Alstrovoks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbario, J., Benton, J. Binnage, H. C., Are, J. R., Ayele, M., Banks, T., Barbario, J. Benton, J. Binnage, H. C., Are, J. R., Ayele, M., Banks, T., Barbario, D. Bouck, J., Benton, J. Binnage, K., Blankenburg, K., Bonnin, D., Carron, T. E., Carter, M. Cavacso, S. R., Chacko, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Joudah, S., Martin, R., Martin, R.
                             HTG 09-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (22-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 187697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
  ACUD 3429

187697 bp DNA linear HTG 09-MAY-200
HOMO Sapiens chromosome 3 clone RP11-64L3, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 187697)
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On Apr 28, 2002 this sequence version replaced gi:16117928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine
Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Project Information
                                                                                                                                         AC063929.15 GI:20335598
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Worley, K.C.
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                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                  Homo sapiens
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                                                     DEFINITION
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TITLE
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KEYWORDS
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TITLE

COMMENT

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/clone_lib∵"RPCI-11 Human Male BAC"
4356. .4523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family."tRNA-Glu-GAG"
2584. .12885
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                                                                                                                                                    /organism≔"Homo sapiens"
/db_xref∵"taxon:9606"
                                                                                                                                                                                                                                                                                                                                              .4906)
                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family."AluJ/FRAM"
                                                      Center clone name: 661_A_3
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4482. .24545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_familyo"AluSg/x"
26165. .26219
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18705. 19009
/rpt_family "AluSx"
complement(20040. 20
/rpt_family "MIR"
20313. 20612
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24360, .2430
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22622. .22652
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32024. .32771
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11059. .11102
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2218. 12291
                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   /rpt_family "HAL1b"
complement(4625...49
                                                                                                                                                                                                                                                                                                                                                                  /rpt_family…"AluJo"
3941 .9014
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[6513. 16567
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20813. .21145
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/rpt_family:"(TA)n"
complement(26405. .2
                                                                                                                                                                                                                                                   /clone~"RP11-661A3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "L1MCc"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11059. .11102
/rpt_family~"L3"
complement(11461.
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.6626. .16926
                                Center project name:
                                                                                                                                                                                                   /chromosome "8"
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2708. .22812
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31240. .31487
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1488. .31862
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18349. 18494
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25673
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11923. .3200
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27947. .2803
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                                                                                                        FEATURES
                                                                                                                                                                                                                                                                              Unpublished
Unpublished
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E (Dases 1 to 20186)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamach, A., Karatas, A., Kells, C., Larkcoque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
Marduls, M., McEwan, P., McKernan, K., McPheters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, J.,
Oliver, J., Petta, R., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Kise, C., Kagoy, P.,
Scham, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
Stojanovic, N., Strauss, N., Sutraus, S., Schauer, S., Schupack, S.,
Young, J., Topham, K., Travers, M., Traigilio, J., Ye, W. J.,
Young, G., Zalinoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young, G., Zalmoun, J., ZemDek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (20-JUL-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 20186)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, M., Bastien, Y., Bloom, T., Boguslawkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chargo, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., Dakrellano, K., Dewark, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Gradyna, S., Ginde, S., Gord, S., Goyette, M., Gage, D., Johnson, R., Jones, C., Kamtz, A., Karatas, A., Kells, C., LaRocque K., Landers, T., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Machan, C., MacChan, C., MacChan, P., Marquis, N., Matthews, C., McCarthy, M., MacGwald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., MacGwald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., MacGwald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., MacGwald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Morman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, R., Phunkhan, P., Pierre, M., Schuer, S., Schuer, S., Schuer, S., Schuer, S., Schuer, S., Schuer, S., Schueback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, V., Strauss, N., Subramanian, A., Talamas, J., Tregfaye, S., Young, G., Zainoun, J., Zambk, L., Zimmer, A. and Zody, M.
Direct Submission
L. Samtted (06-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA
All repeats were identified using RepeatMasker; html
                                                                                                                            Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 201886)
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Homo sapiens chromosome 8, clone RP11-661A3, complete sequence AC092700
                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-661A3 Unpublished
                                                    AC092700.2 GI:21327455
                                                                                                        human.
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/rpt_family∵"MER21B" 32826. .33568

repeat_region

repeat_region

Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

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Editoria, Bertazoa, Unicotasi, Catarrinii, Hominides, Buleacostomi; Mammalia, Eutheria, Primatea; Catarrinii, Hominides, Buleacostomi; Mammalia, Eutheria, Primatea; Catarrinii, Hominides, Buleacostomi; Maron, Adams, C., Adio-Odola, B., Ali-Osman, F. R., Allen, C., Alabrooks, S. L., Amaratuoge, H. C., Are, J. R., Banks, T., Barbaria, J., Banton, J., Bimage, K., Blahkenburg, K., Bonnin, D., Bouck, J., Burket, C., Burrell, R.L., Byrd, N.C., Carron, T. Burket, C., Burrell, R.L., Byrd, N.C., Carron, T. Cond. C., Chiu, D., Chowdhy, J., Chistopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., Delagado, O., Danket, C., Dinh, H. W., Douthwaite, K. J. Delagado, C., Davy-Carroll, L., Dedarich, D. A., Delaney, K. R., Delagado, C., Emerling, S., Escotto, M. Falls, T. Ferragato, D., Edwards, C. C., Elpaj, C., Emerling, S., Escotto, M. Falls, T. Ferragato, D., Edward, C.C., Garier, A., Garier, T., Garier, P., Hart, M., Havlak, P., Hamilton, K., Hant, M., Havlak, P., Hamilton, K., Hant, M., Havlak, P., Hamilton, K., Hart, M., Havlak, P., Hamilton, K., Hant, M., Havlak, P., Howard, S., Huber, J., Lohlay, C., Edit, J., Liu, J., Lichtage, A., Hernandez, J., Hernandez, J., Howard, S., Huber, J., Lohlay, C., Liu, J., Liu, M., Lozado, R., Johnson, B., Jia, Y., Johnson, P., Marcinez, C., Liu, J., Liu, J., Lichtage, C., Lieu, J., Liu, M., Mai, G., Marcinez, M., Maller, R., Martine, E., Mascher, M., Maller, A., Martine, P., Martindale, A., Martindale, M., Martine, P., Martindale, M., Martinda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (30-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 205952)
                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  AC024940.39 GI:15809076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 205952)
Worley, K.C.
Direct Submission
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Worley, K.C.
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Homo sapiens 12 BAC RP11-627K11 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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tive 0; Mismatches 0; Indels 0
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complement (42668. .42807)
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complement (43919. .44010)
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complement(40213..42148)
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                                                                                                                                                                                                                                                                                                           STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and CDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                 entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
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Anote="overlaps bases 104273. .106277 of clone AC068792"
/function="clone overlap"
                                                                                                                           CLONE LENGIH: This sequence does not necessarily represent the
Baylor Plaza, Houston, TX 77030, USA
On Sep 30, 2001 this sequence version replaced gi:15799479.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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complement(1105. .1412)
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complement(1413. .1679)
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1706. .1987
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/chromosome⇔"12"
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complement(3517. .3760)
/rpt_family="Alusx"
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2189. .2400
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1988, .2016
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                                                                           gc-help@bcm.tmc.edu
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1982 GGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAG 2041
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100.0%; Pred. No. 3.7e-27;
ative 0; Mismatches ^ ^.
                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family."AluY"
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complement(8838. 8993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name."103578"
9206. 9338
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complement(9422. 9506)
/rpt_family."L2"
complement(9560. 9858)
                                                                                                                                                                                                                                                                        /rpt_family | Alusx | 7151, 7185
                                                                                                                                                                                                         /rpt_family="AluJo"
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9177. 9471
                                                                          /rpt_family."AluSq"
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                                                                                                                                                                                                                                                               /rpt_family."AT_rich" complement(6416. .670
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                                                                                                                                                                                                                                                                                                                                                            /rpt_family="AluJb"
complement(7649. .7
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                                                                                                                              /rpt_family∵"L2"
                                                               /rpt_family "L2"
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complement(5833.
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                                                                                 complement (5131
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of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)
On Dec 3, 2001 this sequence version replaced gi:16303291.
Location/Qualifiers
                                                                                                                                                                                                                                                                                  45004282 Linear PRI 04-DEC-2001 AP004282
                                                                        1982 GGCACCTGTAAATCCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAG 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens DNA chromosome 8 SEQUENCE
Published Only in Database (2001)
2 (Dases I to 250681)
Shimizu, N. and Asakawa, S.
Direct Submission
Submitted (18-0CT-2001) Nobuyoshi Shimizu, Kejo University, School
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                      Gaps
                                    .;
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens pre-pro-B cell cell_line:FLEB 14 - 14 DNA clone_lib:Keio BAC library clone:KB1165G2.
                                    Indels
                  Pred. No. 3.7e-27; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clb="KB1165G2"
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/cell_type="pre-pro-B cell"
/clone_lib="Keto BAC library"
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/evidence=not_experimental
/rpt_family="AluSx"
complement(697 .880)
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complement(2201. .2433)
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1869. 2159
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/rpt_family="L2"
3696. .3992
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100.08; Pr.
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                  Best Local Similarity 100.
Matches 74; Conservative
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                  RESULT 86
AP004282
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Direct Submission

Submitted (30-APR-2001) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

On May 2, 2001 this sequence version replaced gi:9755791.
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [base] 1 to 228652] Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Gyapay, G., Saurin, W. and Weissenbach, J. Sequencing of the human chromosome 14 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : C-2324M15
Downstream BAC (overlapping the SP6 end) : R-75014 (AC=AL355074)
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175249. .175398
/note="matching EMBL:W60094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identified using the e-PCR software (G. Schuler)"
66543 a 47502 c 47687 g 66920 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percentage of bases with a quality value >= 40 : 99 %.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9; Length 228652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 2.0
Quality coverage: 6.64x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                   Center: Genoscope / Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dbsTs:STS20509
Identified using the e-PCR software (G.
173837. .174009
                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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70246. .70378
/note="matching EMBL:G07509
RHdb:RH95526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="matching EMBL: H49894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens'
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHdb:RH44767
dbSTS:STS37835
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Range : bases
                                                                                                                                                                                                              (bases 1 to 228652)
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AUTHORS
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JOURNAL
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/evidence-not_experimental /rpt_family-"AluSq" 2351023619 /evidence-not_experimental /rpt_family-"MIR" 23817 24117	/ovidencenot_experimental /rpt_family*Alusq." complement(2412124252) /evidence-not_experimental	/fpc_family_wirk complement(24667, .24959) /evidence-not_experimental //rpt_family_wirk complement(26086, .26158)	/evidence=not_experimental /rpt_family="L2" 26183 . 26303 / /evidence=not_experimental /rpt_family="MIR"	2630326613 /evidence=not_experimental /rpt_family="AluJb" 2661426704 /evidence=not_experimental	/rpt_ramily."MIR" 26707 26891 /evidence-not_experimental /rpt_family."MIR" complement(2753328017)	/evidence=noC_experimental /rpt_family."LTR35 complement(2807828837) /evidence=noC_experimental /rpt_familv."TTRRA."	29031 29346 /evidence·not_experimental /rpt_family·*AluJo* 29349 29660 /evidence·not_experimental	/rpt_family="Alujb" complement(29674, .29730) /evidence=not_experimental /rpt_family="L2" 29731, .29780	/evidence-not_experimental /rpt_family."(CA)n" complement(2978130315) /evidence-not_experimental /rpt_family."L2"	complement(3104431338) /evidence=not_experimental /rpt_family="AluSq" 3149731664 /evidence=not_experimental	/rpt_family."HAL1" 3166531944 316653194 /rpt_family."AluSp" 3194531968	/evidence-not_experimental /rpt_family."(CA)n" 3196932285 /evidence-not_experimental /rpt_family."AluY" 322863264 /evidence-not_experimental /rpt_family."HALl"
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Gaps

Query Match 2.6%; Score 74; DB 9; Length 250681; Best Local Similarity 100.0%; Pred. No. 3.7e-27; Matches 74; Conservative 0; Mismatches 0; Indels 0;

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2290. .2586
/hote="AluSx repeat: matches 1. .301 of consensus"
2880. .3136
/hote="MLTIC repeat: matches 191. .464 of consensus"
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5357. 5580
/note="MER4-internal repeat: matches 4806. 6115 of
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'note="FLAM_C repeat: matches 1. .131 of consensus"
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700ce="ILTR8 repeat: matches 444. 584 of consensus"
700ce="AluY repeat: matches 1. 303 of consensus"
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'note="MER4-internal repeat: matches 2321. .5179 of
                          'note="MER58A repeat: matches 2. .223 of consensus"
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6718. 7027
/note="AluSc repeat: matches 1. .303 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluJb repeat: matches 1. .300 of consensus"
complement(11844. .12204)
/note="match: GSS: Em:AQ253047"
12346. .12549
                                                                             .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .291 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .239 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        .444 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1342. .4400
/note="MER4-internal repeat: matches 6115. .6171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consensus"
4401. .5356
/note="LTR25-internal repeat: matches 5493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8444. .8742
/note="AluSx repeat: matches 1.
8880. .9166
/001c="AluY repeat: matches 16.
9252. .9560
/note="AluSx repeat: matches 1.
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| hote="L2 repeat: matches 2659.
| 11170. 11339
| hote="MIR repeat: matches 75. .
| 11418. 11702
                                                                             'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10083. .10388
/note="AluSq repeat: matches 1.
11102. .11153
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1758. .12052
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13150. .14317
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/note="LTR8 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4005. .4217)
/note="match: GSS: Em:AQ209273"
complement(4016. .4252)
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13007. .13103
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                                                                                                                    /note="match: GSS: Em:AQ177716"
1826. 1959
                                                                                                       complement(1337
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/note="MER3 rel
14395. .14691
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Submitted (03-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestics: clonerquest@sanger.ac.uk

On Jul 4, 2001 this sequence version replaced gi:13751511.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSRROT; Tr:, TREMBL; Wp; WORMEPE; Information on the WORMPEP
                             Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm htm VECTOR: page 5. May be a Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: page 6. May be sequence is not the entire insert of clone RPI1-7K24 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RPI1-7K3 is at 1 in this sequence. The true left end of clone RPI1-13908 is at 77320 in this sequence. The true right end of clone RPI1-533020 is at 40694 in this sequence.
CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGG 2045
                                                                                                                                                                                                                                                                              AL512274 79319 bp DNA linear PRI 03-JUL-2001 Human DNA sequence from clone RPI1-7K24 on chromosome 6, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="match: GSS: Em:AQ135411"
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                                                                                                                            AL512274.9 GI:14596369
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Hall, R.
                                                                                                  2046 AGGTTGCAGTAAGC 2059
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                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                           ACCESSION
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KEYWORDS
                                                                                                                                                                                                                            RESULT 87
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/ Anotes "Alusy repeat: matches 1. .298 of consensus" / Anotes "Alusy repeat: matches 1. .298 of consensus" / Anotes "Alusy repeat: matches 5. .135 of consensus" / Anotes "Alusy repeat: matches 7. .312 of consensus" / Anotes "Alusy repeat: matches 7. .312 of consensus" / Anotes "Sequence from overlapping clone RP11-533020 / AL513008). Assembly confirmed by restriction digest." / Anotes "match: GSS: Em:AQ770255" / Anotes "Alusy repeat: matches 1. .291 of consensus" / Anotes "Alusy repeat: matches 1. .313 of consensus" / Anotes "Alusy repeat: matches 1. .313 of consensus" / Anotes "Alusy repeat: matches 1. .313 of consensus" / Anotes "Limics repeat: matches 1. .313 of consensus" / Anotes "Limics repeat: matches 7779. .7929 of consensus" / Anotes "Limics repeat: matches 7779. .7929 of consensus" / Anotes "Limics repeat: matches 7779. .7929 of consensus" / Anotes "Limics repeat: matches 7779. .7929 of consensus" / Anotes "Limics repeat: matches 7779. .7929 of consensus" / Anotes "Limics repeat: matches 7779. .7929 of consensus" / Anotes "Limics repeat: matches 7779. .7929 of consensus" / Anotes "Limics repeat: matches 7779. .7929 of consensus" / Anotes "Limics repeat: matches 7779. .7929 of consensus" / Anotes "Limics repeat: matches 7779. .7929 of consensus" / Anotes "Anotes "
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/note="Aluyb repeat: matches 1. .143 of consensus" 26082. .26209
/note="Limb3 repeat: matches 7612. .7740 of consensus"
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16527. .26826
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27450. .27589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"AluSg/x repeat: matches 72. .299 of consensus"
21946. .22243
                                                                                                                                                                                                                /note="MIR repeat: matches 34. .232 of consensus"
1672. .16872
//note="LiM4 repeat: matches 5718. .5824 of consensus"
16906. .17210
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7897. .28025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="17 copies 2 mer gt 94% conserved"
25394. .25537
25386. repeat: matches 143. .284 of consensus"
25388. .25856
                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L2 repeat: matches 1901. .2748 of consensus"
[8198. .18327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="FLAM_A repeat: matches 1. .133 of consensus" 1828. 18627
18328. 18627
100te="L2 repeat: matches 1614. .1901 of consensus" 18722. 19023
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28089. .28389
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28493. .28610
.137 of consensus"
                              14816. .15150
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20116. .20420
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26827. .26988
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28485. .28537
                                                                                                                                           .310 of
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16190. .16382
'notee" MER3 repeat: matches 18.
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Query Match
2.6%; Score 73; DB 9; Length 79319;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1982 GCGCACCTGTAATCCCAGGTACTTGGGGGGGGGGGGAGAATGGCTTGAACCCAGGG 2041
70901 GGCACCTGTAATCCCAGCTACTTGGGGGGGGGGAATCGCTTGAACCCAGGG 70960

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Lifect Submission

Lifect Submission

Lifect Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 96165)

Burnan, Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Brom, A., Camarata, J., Campoplano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Gerelra, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Govette, M., Graham, L., Grand-Pletre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Kartas, A., Landerde, K., Lamazaries, R.,
Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
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Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Plerre, N., Pollara, V.,
Raymond, C., Rette, R., Rieback, M., Santos, R., Schupback, R.,
Saman, J., Rosetti, M., Roy, A., Santos, R., Schupback, S., Theodore, J.,
Travers, N., Subramanian, A., Travers, M., Travers, M., Travers, M., Travers, M., Vell, R., Vo, A., Milson, B., Wu, X., Tralgillo, J., Ye, W.J., Younq, G.,
Painon, J., Ye, W., Santos, M., Santos, M., Yeil, R., Vo, A., Wilson, D., Ye, W.J., Younq, G., Birren, B. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barker, J., Baladin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colagaelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewai, K., Dowle, M., Ferreira, P., FitzHugh, W., Foriest, C., Funke, R., Gage, D., Galagan, J., Cardyon, S., Gilbert, D., Grant, G., Funke, R., Gage, D., Galagan, J., Cardyon, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Jones, C., Kann, L., Kartas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaudhlin, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Scvery, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Testaye, J., Wuller, J., Wasslliev, H., Vo, A., Waqner, A., Wheeler, J., Wuller, J., Wyman, D., Ye, W.J. and Zody, M. PRI 17-MAY-2002 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Bogus davkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chanqu, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymorr, A., Cooka, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidac, Homo. Zalnoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center to Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA ACUU9702 96165 bp DNA linear Homo sapiens, clone RP11-197111, complete sequence. AC009702 1 (bases 1 to 96165)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo, Sapiens, clone RP11-197111 11111111111 70961 GTGGAGGTTGCAG 70973 2042 GTGGAGGTTGCAG 2054 Direct Submission Homo sapiens. AC009702.12 Homo sapiens Unpublished DEFINITION ACCESSION ORGANISM TITLE JOURNAL REFERENCE REFERENCE AUTHORS TITLE JOURNAL TITLE JOURNAL REFERENCE AUTHORS VERSION KEYWORDS SOURCE RESULT 88 AUTHORS REFERENCE AUTHORS AC009702 LOCUS q ò

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7765. .1797^4
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13845. 13897
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13939. 13991
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[4001. .14142
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15420 15440
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complement(17447.
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                                                                                                                      /rpt_family="5s"
9410. .9589
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:0478. .20704
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Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
McCarthy,M., McEvan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Raymond,C., Retta,R., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Direct Submission
London,J., Cambek,L., Zimmer,A. and Zody,M.
Submitted (17-MAY-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 0214, USA
On May 17, 2002 this sequence version replaced g1:20128778.
All repeats were identified using Repeatmasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/Repeatmasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Only the last 96.2 kilobases of this clone are being submitted. The remainder overlaps accession number AC021915 [WICGR project L4214].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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complement(2926. .3341)
/rpt_family="LTR16"
complement(2926. .3290)
/rpt_family="LTR16A"
complement(3471. .3684)
/rpt_family="LL"
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/db_xref="taxon:9606"
/clone="RP11-197111"
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/rpt_family="MLT1B"
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/rpt_family="MIR"
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complement(6567, .6698)
/rpt_family="MER31-int"
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/rpt_family="MER92C"
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456. .5592
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5876. .6185
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613. .5700
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7355. 7547
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/rpt_family="AluJb"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Waligorski,J., Abbott.A. and Boyer,E.
The sequence of Homo sapiens BAC clone RP11-475H17
Unpublished
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100.0%; Pred. No. 1.2e-26;
Live 0; Mismatches 0;
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42855 a 28390 c 27230 g 42380 t
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105059, .122694
/note assembly_fragment"
122795, .141175
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Sulston, J.E. and Waterston, R.
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94003. .104958
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Waterston, R. H.
Direct Submission
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Mommalish Euthberia; Primates; Catarrhini; Hominidae; Homo.

Bitrenb. 1. Linton.L., Nusbaum,C. and Lander.E.

Homo sapiens chromosome, clone RPII-45N3

E. Chaesa It of 14175)

By Hirab. 1. Linton.L., Nusbaum,C., Lander.E., Allen,N., Anderson,M., Balddrin,J., Bauthgalter.B.,

By Hirab. 2. Linton.L., Doyle,M.,

Cooke, P. DeArallano,K. Colangelo,M., Collymore,A., Cooke,P. DeArallano,K., Porrest.C., Hagos,B., Headondan.L., Doyle,M.,

Perraira.P., Castle,M., Colangelo,M., Collymore,A., Machan,J., Cooke,B., DeArallano,K., Machandan,E., Doyle,M.,

Perraira.P., Cardyna,S., Granic,G., Hagos,B., Headondan,L.,

Englagan,J., Cardyna,C., Cacke,K., Machandan,P., Martan,B.,

Engladan,J., Candon,C., Cacke,K., Machandan,P., Doyle,M.,

Perraira.P., Machan,S., Granic,G., Hagos,B., Headondan,L.,

Englagan,J., Cardyna,C., Cacke,K., Machandan,P., Doyle,M.,

Engladan,J., Cardyna,C., Gooke,K., Mann,L., Karatas,A., Machan,L.,

Engladan,J., Maylor,J., Latu,C., Locke,K., Machanda,P., Martan,B.,

Machan,J., Maylor,J., Latu,C., Locke,K., Machanda,P., Martan,B.,

Englagan,P., Mockernan, K., Machanda,P., Martan,B.,

Englagan,J., Maylor,J., Latu,C., Locke,K., Mann,L., Karatas,A., Machan,

Martan,D., Ye,W.J., Zimmer,A., Stolanovico, N., Stolanovico, Stonaca, Martan,B., Stolanovico, Stonaca,B., Stonaca,B., Martan,B., Martan,B.
                                                                                                                     HTG 10-NOV-2000
                                                                                                                   AC012110 141175 bp DNA linear HTG 10-NOV-200
Homo sapiens clone RP11-45N3, WORKING DRAFT SEQUENCE, 4 unordered
                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                       AC012110.4 GI:11136803
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens.
HOMO sapiens
  7255 TGGAGGTTGCAGT 7267
                                                                                                                 AC012110
                                                                                                                                      DEFINITION
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COMMENT

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VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-471D6; the clone sequenced to the right is RP11-479L11, 200 bp overlap. Actual end of this clone is at base position 49393 of RP11-479L11.
Submitted (09-AUG-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 6 (bases 1 to 144355) Waterston, R.
                                                                                  Direct Submission
Submitted (Or)NOV-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 24, 2001 this sequence version replaced gi:13270791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this folore. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one
                                                                                                                                                                     Center: Washington University Genome Sequencing Center
Center code: WGGSC
                                                                                                                                                                                                                          1. .144355
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/db_xref="taxon:9606"
/chromosome="2"
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405. .445
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                                                                                      TITLE
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                                                                  AUTHORS
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Submitted (15-FEB-2000) Whitehead Institute/MIT Center tor Genome
                            Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 6, 2001 this sequence version replaced gi:13184166.
All repeats were identified using RepeatMasker:
Smit, A.F.A. 6 Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                            Center project name: 139_0_23

Center clone name: 139_0_23

Sequencing vector: M3: M7815: 2% of reads
Sequencing vector: Plasmid: n/a: 98% of reads
Sequencing vector: Plasmid: n/a: 98% of reads
Sequencing vector: Plasmid: n/a: 98% of reads
Assembly program: Phrap: version 0.960731
Consensus quality: 153109 bases at least 040
Consensus quality: 154194 bases at least 040
Consensus quality: 154534 bases at least 020
Insert size: 157000: agarose-fp
Insert size: 157000: agarose-fp
Ouality coverage: 11.3 in 020 bases; agarose-fp
Ouality coverage: 11.4 in 020

* NOTE: This is a "working draft' sequence: It currently
consists of 8 contigs. The true order of the pieces
is not known and their order in this sequence record
is not known and their order in this sequence record
is arbitrary. Gaps between the contigs are raprosented as
iruns of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will

be preserved.
                                                                                                                                                                                                                                                                                Contact: sequence_submissions@qenome.wi.mit.edu
------- Project Information
Center project name: L5446
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59571 79596: contig of 20026 bp in length
79597 79696: gap of 100 bp
79697 100382: contig of 29686 bp in length
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                                                                                                                                                                                                                            Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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Homo sapiens chromosome 8 clone RP11-219D23 map 8, WORKING DRAFT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG: HTGS_PHASE1; HTGS_FULLTOP.
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1 Similarity 100.0%; Pred. No. 1.2e-2
73; Conservative 0; Mismatches
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/rpt_family="11"
43511. 43812
/rpt_family="ERVL"
44561. 4462
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47176. .48678
/rpt_family="L1"
                                                                    /rpt_family~"ERVL"
43211. .43510
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/4633. .452=7
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45358. .46188
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46874, .460co
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42828. .43210
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16279, .46514
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Submitted (13-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Sulston, J. E. and Waterston, R.
                                                                                                                                                                                                          1983 GCACCTGTAATCCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCCAGGAGG
                                                                                                                                                                          Gaps
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Homo sapiens BAC clone RP11-153B21 from 2, complete sequence.
AC009305
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On Aug 19, 2000 this sequence version replaced gi:5732166.
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                                                                                                                                  Length 155378;
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The sequence of Homo sapiens BAC clone RP11-153B21
Unpublished
                                                                        700 others
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Contact: sapiens@watson.wustl.edu
                                                                                                                                                    1.2e-26;
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                                                                                                                                  2.6%; Score 73; DB 2;
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| 30633 c 30876 g 46276 t
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                /note="assembly_fragment
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145266. .155378
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Waterston, R.H.
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                                      clone_end:T7
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa.K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEIGHBOAN DATA SEQUENCE INFORMATION:
The clone sequenced to the left is RPI1-541A15; the clone sequenced to the right is RPI1-62F14. Actual start of this clone is at base position 1 of RPI1-153B21; actual end is at base position 167116 of RPI1-153B21.
                                                                                                                                                                                                                                                                                                                                                                    Louis
This sequence may not represent the entire insert of this
                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                    clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                      Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. LMO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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7178. 7486
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
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11566. .11866
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1483. .2196
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/rpt_family="L1"
9924. .9981
/rpt_family="MIR"
10061. .101er
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10222. 10383
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11425. .11565
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ACU/9360 176176 bp DNA linear HTG 31-JUL-2002
Homo sapiens chromosome 12 clone RP11-7M8, WORKING DRAFT SEQUENCE,
12 unordered pieces.
                                                                                    1983 GCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGG
                                                               0;
                                        Length 167116;
                               Score 73; DB 9; Length 1673; Pred, No. 1.26-26;
                                                                                                                                                                                                                                          AC079360.22 GI:22002362
HTG; HTGS_PHASE1; HTGS_FULLTOP.
                                            100.0%; Pred. no.
/rpt_family."L2"
37939. .37974
/rpt_family."(TGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 176176)
                                                                                                                                         2.68;
                                                                                                                             2043 TGGAGGTTGCAGT 2055
                                                              73; Conservative
                                                     Best Local Similarity
                                                                                                                                                                                                                                                                            Homo sapiens
             repeat_region
                                          Query Match
                                                                                                                                                                                                             DEFINITION
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                                                               Matches
                                                                                                                                                                               RESULT 93
AC079360
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                                                                                                                                                                                                                                                                                                                                                                     to EST AA426194 (NID:92107534) zwllf02.rl"
                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Ll"
27814. .28226
2825. argin to EST AI867228 (NID:g5540244) wa01f10.xl"
28785. .29014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3083. .3438
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34097. .3440
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34411. .3451
        /rpt_family="MER1_type"
[2108, 12263
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13912. .14201
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35714. 36147
/rpt_family="MER2_type"
37176. 37360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family~"MER2_type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MaLR"
33026. .33116
/rpt_family="L1"
33268. .33291
/rpt_family="AT_rich"
33382. .33635
                                                                                                                                                                                                                                                                                 /rpt_family="L1"
20554. .21109
/rpt_family="LTR19B"
23356. .23414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_femily="11"
30587 .30882
/rpt_femily="0ther"
31514 .31907
7rpt_femily="11"
31982 .32649
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29015. .29301
/rpt_family="Alu"
29302. .30552
                                                                                                                                     rpt_family="MaLR"
7028. .17219
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9813. .190>°
                                                 /rpt_family="Alu"
14588. .14891
                                                             /rpt_familye"Alu" (4893. .1501'
                                                                                                                                                                                                                     rpt_family="Alu"
9495, .19801
                                                                                                                                                                            rpt_family="Alu"
8232. .18533
                                                                                                                                                      rpt_family="L1"
7705. .18003
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5792. .25889
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6248. .16622
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6654. .16969
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8740. .18966
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2650. .33025
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5402. .35564
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AL162211 179470 bp DNA linear HTG 10-JUL-2001
Homo sapiens chromosome 13 clone RP11-157H17, *** SEQUENCING IN
PROGRESS ***, 16 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179470)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 21, 2000 this sequence version replaced gi:9212905.
                                                                                                                                     1983 GCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Consensus quality: 170263 bases at least Q40
Consensus quality: 173209 bases at least Q30
Consensus quality: 175040 bases at least Q30
Insert size: 177970; sum-of-contigs
Insert size: 218642; 8.2% error; agarose-fp
Quality coverage: 3.74x in Q20 bases; sum-of-contigs Quality
coverage: 3.12x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is a true of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                           0;
                                                  Length 176176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 24720 bp in length
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79206: contig of 22392 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20112 20211: gap of 100 bp
20212 22684: contig of 2473 bp in length
22685 22784: gap of 100 bp
22785 26050: contig of 3266 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p of 100 bp contig of 5744 bp in length
                                                                       1.2e-26;
                                                Score 73; DB 2;
Pred No. 1.2e-2
                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_CANCELLED
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                                                  2.0,,
100.0%; Pre
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                                                                                                                                                                                                                          2043 TGGAGGTTGCAGT 2055
                                                                                           Conservative
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                  Local Similarity
nes 73; Conser
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AL162211.5
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             Direct Submission

Submitted (29-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Submission

Submitted (31-JUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 29, 2002 this sequence version replaced gi:19718706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                Department
                                                                                                                                                                                Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ordenistry: Dye-trimer Bodipy: 18% of reads
Chemistry: Dye-terminator Big Dye: 87% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 169109 bases at least 040
Consensus quality: 171607 bases at least 030
Consensus quality: 173502 bases at least 030
Estimated insert size: 163861; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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gap of unknown length
contig of 2573 bp in length
gap of unknown length
contig of 2349 bp in length
gap of unknown length
contig of 2415 bp in length
gap of unknown length
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contig of 8128 bp in length
gap of unknown length
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of 5723 bp in length
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contig of 8102 bp in length
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                                                                                                                                                                                                                                                                                                        Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
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/db_xref="taxon:9606"
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us-09-966-880a-7.100olig.rge

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112649 112748; gap of 13874 bp in tengun 112649 112748; gap of 100 bp 112749 126894; contig of 14146 bp in length 112689 126894; contig of 14146 bp in length 126895 126894; contig of 13442 bp in length 140437 140536; gap of 100 bp 140537 140536; gap of 100 bp 148269 148368; contig of 7732 bp in length 148369 148368; contig of 2879 bp in length 151248 151347; contig of 2879 bp in length 151348 160829; contig of 9482 bp in length 160830 160829; gap of 100 bp 160829; gap of 160930 179470; contig of 18541 bp in length.
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/note="assembly_fragment:00269"
ture 160930. .179470
/note="assembly_fragment:00989"
54009 a 35515 c 34477 g 53955 t 1514 others
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98674: contig of 11658 bp in length
98774: gap of 100 bp
112648: contig of 13874 bp in length
82214: contig of 2908 bp in length
                     14: gap of 100 bp
86916: contig of 4602 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-11.1"
| . 2011|
| . . 2011|
| / other_assembly_fragment:01022
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| fragment_chain:1"
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| fragment_chain:1"
| / other_assembly_fragment:00208
| fragment_chain:2"
| / other_assembly_fragment:01315
| fragment_chain:2"
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98775. 112648
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112749. 126894
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140537. 148268
140537. .148268
140537. .148268
140537. .148268
140537. .148268
140537. .148268
140537. .148268
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79307. .Room
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/note-"assembly_fragment:00835
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82315. .86916
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/db_xref="taxon:9606"
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/clone="RP11-157H17"
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                        82314
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87017
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ORIGIN
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Direct Submission

Direct Submission

Direct Submission

Burner Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Burner, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Choapel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Money, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gorde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Johnson, R., Johnson, S., Gorde, S., Cooke, M., Iliev, I., Johnson, R., Johnson, C., Machen, P., Malls, C., LaRocque, K., Lamazarus, R., Landers, T., Lehockky, J., Levine, Y., Marquis, N., Methwes, C., Macdonald, P., Major, J., Marquis, N., Methwes, C., Macdonald, P., Major, J., Marquis, N., Methwes, C., Nicol, K., Morbu, C., Norman, C.H., O'Conner, T., O'Donnell, P., O'Donnell, P., O'Donnell, P., Schauer, S., Schupback, K., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Topham, K., Travers, M., Travers, N., Travers, N., Travers, N., Vell, N., Vell
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                                                                                                                                                                                                                                                                                                                                      ACO21915 183101 bp DNA linear PRI 30-APR-2002
Homo sapiens chromosome 8, clone RPl1-26M5, complete sequence.
ACO21915
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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O
                              Length 179470;
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                                                                                                1.2e-26;
                                    Score 73; DB 2;
Pred. No. 1.2e-2
2.6%; Suc. 100.0%; Pred. No. .. .. .. 0; Mismatches ... 0; Mismatches ... ... 0; Mismatches ... ... 0; Mismatches ... 0;
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Matches 73; Conservative
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         Luted (10-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases I to 183101)

Biren,B. Linton,L. Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Buckhgalter,B. Brown,A., Camparata,J., Campoplano,A., Chang,J.,

Choepel,T., Colangelo,M., Collins,S., Chang,J.,

Choek,B., Choepel,T., Colangelo,M., Collins,S., Collymore,A.,

Cook,A., Cook,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,

Faro,S., Ferreira,P., FitzHugh,W., Gapg,D., Galagan,J., Gardyna,S.,

Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

Hagos,B., Horton,L., Hulme,W., Illev,I., Johnson,R., Jones,C.,

Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lanazares,R.,

Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,

MacLean,C., Morton,L., Murphy,T., Naylor,J., Marquis,N., Mathews,C.,

Minova,T., MacMonald,P., Major,J., Marquis,N., Mathews,C.,

Minova,T., Mlenga,V., Murphy,T., Naylor,J., Marchi,L.D.,

Oliver,J., Peterson,K., Phukhan,P., Pierre,N., Pollara,V.,

Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,

Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,

Seaman,S., Severy,P., Spencer,B., Schupback,S., Theodore,J.,

Yoll,R., Vo,A., Wilson,B., Wuu,X., Wiman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

All repeats were identified using Repeatmasker:

Non Apr 10, 2002 this sequence version replaced gi:19681737.

Conter: Whitehead Institute/MIT Center for Genome Research, 320 charles Street, Cambridge, MA 02141, USA

On Apr 10, 2002 this sequence version replaced gi:19681737.

Conter: Whitehead Institute/MIT Center for Genome Center.

Conter: Whitehead Institute/MIT Center for Genome Center.
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Web Site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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complement(648. .857)
/rpt_family="MER2"
858. .1175
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/rpt_family="MIR3"
4631. .4683
/rpt_family="(TCCA)n"
4725. .4759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .183101
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
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complement(1176. .1330)
/rpt_family="MER2"
complement(1457. .1634)
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/rpt_family="GA-rich"
3007. .3172
/rpt_family="AluJo"
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Center clone name: 26_M_5
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/rpt_family="Aluub" complement(11248 .11560) /rpt_family="Aluga" complement(11561 .11676) /rpt_family="Aluga" /rpt_family="Aluub" /1902 .12035 /rpt_family="Aluxb8" 20859. 20915 /rpt_family="Arrich" 21017. 21343 /rpt_family="MLT1J" complement(10194. 10366) /rpt_family="LiME1" 10392. 10567 /rpt_family="MER92B" 10629. 10699 /rpt_family="LrR16A" complement(16479...16821) /rpt_family="MLT1A1" 16904...17291 /rpt_family="MLT1B" complement(19512...19619) complement(13010...13146)
rpt_family="MER91A"
3548...13571 complement(12421. 12726) /rpt_family="AluSg" complement(12902. 12989) /rpt_family="FLAM_A" /rpt_family="MIR" complement(23504. .23679) /rpt_family-"Alusx" 8139. . R424 /rpt_family="MLT1K" complement (8697. .9011)
/rpt_family="Alusx"
complement (9012. .9191)
/rpt_family="MLT1B" complement(9350...9391) /rpt_family="55" .9821) complement(8474. 8696) rpt_family="MER31-int" /rpt_family="AT_rich"
14361. .14453
/rpt_family="MIR"
14918. .15131
/rpt_family="L2"
15261. .15676 /rpt_family="(TG)n" 4991. .5020 /rpt_family="AT_rich" 'rpt_family="LTR16A1" 5312. .15676 rpt_family="MLT1A1" 10629. .10599 /rpt_family="MER92C" complement(11055. .1 rpt_family="FLAM_C" 2698. .22788 3139. .8424 /rpt_family="AluSg" rpt_family="AluSq" rpt_family="(GA)n" 2169. .22307 rpt_family="MIR" 2797. complement (9521. complement (6025

Length 183101;

2.6%; Score 73; DB 9; L 100.0%; Pred. No. 1.2e-26; .502 of consensus"

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//occe="28 copies 2 mer aa 78% conserved"
3237. 3258
3237. 3258
//octe="Limit repeat: matches 10. .214 of consensus"
3268. 3379
//octe="Limit repeat: matches 5592. .6332 of consensus"
//octe="Aulox repeat: matches 2. .293 of consensus"
//oce="Malox repeat: matches 28. .131 of consensus"
//oce="MRR repeat: matches 28. .131 of consensus"
//oce="MRR repeat: matches 68. .185 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"MIR repeat: matches 25. .99 of consonsus"
11947. .12156
/note-"LIPA15 repeat: matches 5940. .6153 of consonsus"
14745. .14978
                                      /note="L1PA16 repeat: matches 3670. .6139 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluSg/x repeat: matches 168. .296 of consensus"
41131. .41428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 7114. .7740 of consensus"
                                                                                                                                                                                                                                                                                                                    /note="12 repeat: matches 2679. 2750 of consensus"
1623. 16413
/note="MrIH repeat: matches 110. 288 of consensus"
1645. 1657
/note="MrIH repeat: matches 382. 495 of consensus"
18920. 19339
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/note="L2 repeat: matches 2641. .2703 of consensus"
34897. 35200
36514. 36545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Alusx repeat: matches 1. .295 of consensus"
20679. .21301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MER5A repeat: matches 1. .188 of consensus" 34815. .34879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"8 copies 4 mer caca 87% conserved"
36746. 36842
7note-"MER46A repeat: matches 1. .97 of consensus"
38934. 39176
                                                                                                                                                                                                                                                                 /note="MIR repeal: matches 32. .262 of consensus"
15709. .15778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"MIR repeat: matches 20. .196 of consensus" 32027. .32082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matches 4. .421 of consensus"
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2548, .42734
                                                           10594. .11173
/note="MLT2CB repeat: matches
11174. .11246
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/note="MSTB repeat:
20087. .20378
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On Feb 8, 2001 this sequence version replaced gi:12580982.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with rolly a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was continued by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; TT:, TREMBL; WP:, WORMPEP; Information on the WORMPEP that their source adabases: Em:, EMBL; Sw:, Company of the continued of the 
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Human DNA sequence from clone RP11-506P24 on chromosome 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chri3
RP11-506P24 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 191652)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the entire insert of clone RP11-506P24 The true left end of clone RP11-157H17 is at 67628 in this sequence. Location/Qualifiers
                                                        1983 GCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGG
        Gaps
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/note="L2_repeat: matches 1901. .2407 of consensus"
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/note="11 copies 4 mer gata 97% conserved"
     Indels
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/organism="Homo sapiens"
/dx_xref="taxon:9606"
/chromosome="13"
/clone="RP11-506p24"
/clone_lib="RPCI-11:2"
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                                                                                                                                                                                                        11347 TGGAGGTTGCAGT 11335
                                                                                                                                                                       2043 TGGAGGTTGCAGT 2055
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   complete sequence.
AL354668
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AL354668/c
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  Matches
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TITLE
JOURNAL
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KEYWORDS
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.4592 of consensus" .3648 of consensus"

.298 of consensus"

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70.00. - 3.7003
70.04. - 57.087
70.04. - 57.087
70.04. - 57.087
70.04. - 57.087
70.04. - 57.087
70.04. - 57.087
70.04. - 12.045 repeat: matches 1. .304 of consensus."
57.088 . .57.374
70.04. - 12.045 repeat: matches 1. .284 of consensus."
58.080 . .583.74
70.04. - 12.045 repeat: matches 4339 . 4980 of consensus."
58.080 . .583.74
70.04. - 12.045 repeat: matches 1. .294 of consensus."
58.080 . .592.1
70.04. - 12.045 repeat: matches 24255 . 4339 of consensus."
58.089 . .592.21
70.04. - 12.042 repeat: matches 2675 . .4268 of consensus."
70.04. - 12.042 repeat: matches 354 . .423 of consensus."
60.098 . .61059
70.04. - 12.042 repeat: matches 354 . .423 of consensus."
61512 . .62087
70.04. - 12.042 repeat: matches -668 . .100 of consensus."
60.053 . .62087
                                            /note="1.1PA6 repeat: matches 4434. .6143 of consensus" 47218 47396 /note="1.1PB3 repeat: matches 5956 6100
                                                                                                                                                                                                                                                                                                                                                                                                        /note="12 repeat: matches 1617. .1753 of consensus" 55409. .56705
//note="LIMAS repeat: matches 5064. .6300 of consensus" 66706. .57003
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/note="L2 repeat: matches 1609, .2750 of consensus" 51426, .51726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2732 of consensus"
                                                                                                                                                                                                                                                                                                                                                 .1530 of consensus"
'note="MADE1 repeat: matches 1. .80 of consensus"
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/note="LIM1 repeat: matches 3067. .5737 of
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                                                                                                                                                                                                                                                                                                                                                                                         LTR29 repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 1199.
51733. .51845
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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188583 GCACCTGTAATCCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGG 188524
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                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Missouri 63108,
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The sequence of Homo sapiens BAC clone RPI1-549B18
Unpublished (2002)
Jeass 1 to 202950)
Waterston, R. H.
Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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Submitted (25-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6:
On Nov 8, 2000 this sequence version replaced gi:7631062.
Center: Washington University Genome Sequencing Center
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Missouri 63
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Park Avenue, St. Louis,
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Park Avenue, St. Louis,
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NHO549B18
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Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Query Match 2.69 Best Local Similarity 100.0 Matches 73; Conservative

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                                                                 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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/note="similar to
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rpt_family="L1"
712. .7017
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'note="similar
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/note="assembly_fragment clone_end:SP6 vector_side:left"
36083. .65042
/note="assembly_fragment"
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17824. .184709
/note="assembly_fragment clone_end:T7 vector_side:left"
184810. .191831
213879 215264 contig of 1386 bp in length
215565 21641 contig of 1077 bp in length.

* NOTE: This is a "working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
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116662. .137695
/note="assembly_fragment"
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/note="assembly_fragment"
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154285. .166582
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191932. .198683
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/db_xref="taxon:9606"
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                                                                                                                                                                                               AP001336 216441 bp DNA linear HTG 19-AUG-2000 Homo sapiens chromosome 18 clone RP11-735F7 map 18q12, WORKING DRAFT SEQUENCE, 18 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Quality coverage: 10.84x in Q20 bases; sum-of-contigs
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Contact: hattori@gsc.riken.go.jp
------ Project Information
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SOURCE
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NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
      Quality coverage: 5.64 in Q20 bases; sum-of-contigs
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Submitted (03-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Catarrhini; Hominidae; Homo.
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On Jul 7, 2000 this sequence version replaced gi:8570009
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Web site:http://genome.wustl.edu/gsc/index.shtml
Center project information
Center project norman HNH0403N24
Sequencing vector: M13; 75%
Sequencing vector: M13; 75%
Chemistry: Dye-primer ET; 75% of reads
Chemistry: Dye-primer ET; 75% of reads
Chemistry: Dye-terminator Big Dye; 25% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 228280 bases at least 040
Consensus quality: 228280 bases at least 030
Consensus quality: 228280 bases at least 020
Insert size: 212000; agarose-fp
Insert size: 213600; agarose-fp
Insert size: 213608; sum-of-contigs
Quality coverage: 5.72 in Q20 bases; agarose-fp
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209927. .212133
/note="assembly_fragment"
21234. .213778
/note="assembly_fragment"
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100.0%; Pred. No. 1.2
:ive 0; Mismatches
              198784. .202513
/note="assembly_fragment"
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Waterston, R.H.
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Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:

Cambridgeshire, CB10 18A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Apr 15, 2002 this sequence version replaced gi:20145365.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em: EMBL; Sw:

SWISSPROT; Tr:, TREMBL; WP: WORNDEP; Information on the WORNDEP
                                                                                                                                                          AL669821 BPI 24-APR-2002 Human DNA sequence from clone XXbac-116A1 on chromosome 6, complete
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from a CHORI-501 human bac - PGF cell line library VECTOR:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 4.1e-26;
Matches 72; Conservative 0; Mismatches 0;
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26990 a 19373 c 19477 g 23371 t
                      Score 73; DB:
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/clone="XXbac-116A1"
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42497 CACCTGTAATCCCAGCTACTTGGGAGGCTGAGCAGGAGAATCGCTTGAACCCAGGAGGT 42556
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                                                                 2044 GGAGGTTGCAGT 2055
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-MODEL-frame+_p2n.model.-PEV=Xlp
-MODEL-frame+_p2n.model.-VEV=Xlp
-Q-Cgn2_1/USPTO_spool/US09966880/runat_16072003_115617_17474/app_query.fasta_1.391
-Q-Cgn2_1/USPTO_spool/US09966880/runat_16072003_115617_17474/app_query.fasta_1.391
-DB-GenEmb1 -QFWT=fastap -SUFFTX=100align.rge -MINAATCH=0.1 -LCOPCL=0
-LOOPEXT=0 -UNITS=blts -GTART=1 -END=-1 -MATRIX=oligo -TRANS=human40.cd1
-LIST=500 -DOCALIGN=200 -THR_SCORE=940ality -THR_MIN=1 -ALIGN=100 -MODE=LCCAL
-USFR=US09966880_@CGN_1_13745_@runat_16072003_115617_17474 -NCPU=6 -ICPU=3
-NO_MANAP -LARGEQUERY -NGE_GCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-EGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
                                                                                                                        July 17, 2003, 20:58:25; Search time 1772 Seconds (without alignments) 3251.894 Million cell updates/sec
                                                                                                                                                                                                                                      MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL 198
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                         nucleic search, using frame_plus_p2n model
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AF529831 Mus muscu
AF529821 Cricetulu
AF529825 Cricetulu
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AF529842 Cricetulu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (b7-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammanla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
Martin, A. and Scharff, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Somatic hypermutation of the AID transgene in B cells and non-B
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Homo sapiens clone Ramos 9 AID (AID) mRNA, partial cds.
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Martin, A. and Scharff, M.D.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Durandy,A. Activation-induced cytidine deaminase (AID) deficiency causes the autosomal recessive form of the Hyper-IgM syndrome (HIGM2) cell 102 (5), 565-575 (2000)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Gupta,J., Ho.S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McCbowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 17 Row: a Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9988409. Location/Qualifiers
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NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
387 c 421 g 499 t
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                                                                                                                     PRI 12-JUL-2001
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1837)
                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (09-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Email: cgapbs-remail.nh.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC).
                                                                                                                   BC006296 1837 bp mRNA linear PRI 12-
Homo sapiens, activation-induced cytidine deaminase, clone
MGC:12911 IMAGE:4054915, mRNA, complete cds.
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/clone_lib="NIH MGC_48"
/lab_host="DH10B-R"
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/db_xref="LocusID:57379"
/db_xref="taxon:9606"
/clone="MGC:12911 IMAGE:4054915"
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/protein_id~"AAM95416.1"
/db_xrefe~"G1:22297246"
/translation~"MDRLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
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NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
                                                                               AF529829 596 bp mRNA linear SYN 19-AUG-2002
Mus musculus clone 2 transgenic Homo sapiens AID (AID) mRNA,
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Sciurognathi; Muridae; Murinae; Mus
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Martin, A. and Scharff, M.D.
Direct Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                                                                                                                                                                                                       non-B cells
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/organism⊶"Homo sapiens"
/db_xref⊶"taxon:9606"
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 596)
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQ1AIMTFKDYFYCWNTFVENHERTFK
AMEGLHBRYLSRQLRRILLPLYFEVDDLRDAFRTLGL"
548 c 55 9 776 t
                       Muto, T. Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T. Direct Submission

Email: Honjo, Kyoto University, Department of Medical Chemistry, Faculty of Medicine; Yoshida, Sakyo-ku, Kyoto, Kyoto 606-8501, Japan (E-mail:honjo@mfour.med.kyoto-u.ac.jp, Tel:81-75-753-4371(ex.4371), Fax:81-75-753-4388)

Location/Qualifiers

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/protein_id="BAB12721.1"
/db_xref="GI:9988410"
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AF529843 597 bp mRNA linear SYN 19-AUG-2002
Cricetulus griseus clone 3 transgenic Homo sapiens AID (AID) mRNA,
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Rodentia, Sciurognathi, Muridae, Cricetinae;
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1 (bases 1 to 597)
Martin,A and Scharff,M.D.
Somatic hypermutation of the AID transgene in
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Martin, A. and Scharff, M.D.
Direct Submission
                                                                                                       US-09-966-880A-8 (1-198) x AF529842
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Eukaryota, Metazoa;
Mammalia, Eutheria;
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NLSLAIFTARLYFCEDRKAEPBGLRRLHRAGYVOIAIMTFKDYFYCWNTFVENHERTFK
AMBGLHENSVRLSRQLRRLLHPLYEVDDLRDAFRTWGR"
167 9 149 t
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2 transgenic Homo sapiens AID (AID) mRNA,
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                                                                                                              GlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeuLeuProLeu 183
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
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                             Cricetulus.

L (bases I to 597)

Martin, A. and Scharff, M.D.

Somatic hypermutation of the AID transgene in B cells and
                                                                                                                                                                                                                                         184 TyrGluValAspAspLeuArgAspAlaPheArgThrLeuGlyLeu 198
                                                                                                                                                                                                                                                    1. .597
/organism="cricetulus griseus"
/db_xref="taxon:10029"
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/db_xref="taxon:9606"
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Cricetulus griseus clone 2
complete cds.
AF529842 GI:22297271
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Cricetulus griseus clone 4 transgenic Homo sapiens AID (AID) mRNA, complete cds.
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NUSLBIFTARLYFCEDRRAEPEGLRRLHRAGYOIAINTFKDYFYCWNTFVENHERTFK
NWEGLHENSVRLSROLRRLLLPLYSVDDLRDAFRTWGR"
1 163 c 148 t
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E 2 (bases 1 to 597)
S Martin, A and Scharff, M.D.
Direct Submission
L Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
rce /organism."Cricetulus griseus"
/db.xrefr."taxon:10029"
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID
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/product~"AID"
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Sciurognathi; Muridae; Cricetinae;
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the
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Eukaryota; Metazoa;
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
                                                                                                                                                                                                                                                                                                                                                linear SYN 19-AUG-2002
sapiens AID (AID) mRNA,
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                                                                                                                                                         AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Cricetinae;
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10461, USA
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                                                                                                                                             AlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThr
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Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
Location/Qualifiers
1. 597
//db_xref="taxon:10029"
//clone="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells
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Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B
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7 transgenic
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/db_xref="G1:22297282"
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/db_xref="taxon:9606"
1. .597
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Rodentia;
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1. .597
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/gene="AID"
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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complete cds.
AF529847
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NABGLHENSVRLSROLRRILLPLYFUDDLRDAFRTWGR"
167 9 147 1
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griseus clone 6 transgenic Homo sapiens AID (AID) mRNA,
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                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Cricelinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 PheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeuPheLeuArgTyrlle 65
                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 597)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-301-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                    and non-B
       481 GCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 MetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArqArg
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Mismatches:
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/organismu"Cricetulus griseus"
/db_xrefr"taxon:10029"
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                                                                                                                                                                         AF529846.1 GI:22297279
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1. .597
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                      Chinese hamster
                                                                                                                                                complete cds.
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Best Local Similarity:
Query Match:
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCRHVADFLRGNP
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AWEGHHENSVRLSRQLRRLLFEYDDLRDAFRTWGR"
164 c 156 g 148 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThr 140
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Direct Submission
Submitted (17-5002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThr
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                   /db_xref="taxon:9606"
1. 597
/gene="AID"
                                                                                                                                                                                                                                                                                    /protein_id~"AAM95439.1"
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                                                                      US-09-966-880A-8 (1-198) x AF529852 (1-597)
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Best Local Similarity:
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Unpublished
Unbases 1 to 596)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-50L-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
1. 596
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B cells and non-B
                                                                                                                                                                                                                                                                                                                         1 MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp
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AF529815.1 GI:22297217
AWEGLHENSVRLSRQLRHILLPLYEVDDLRDAFRTLGL"
164 c 153 g 150 t
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Matches:
Conservative:
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
                                                                                                                                                                                                                                                                                                                                                                                                               mRNA linear SYN 19-AUG-2002
Homo sapiens AID (AID) mRNA,
                                                            255
                                                                                                                                  TyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGlyLeu 165
                                                                                                                                                                                                                                               ProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGlyAsnProAsnLeuSer 105
                                    85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.

Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B and non-B cells
Uppublished
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 SerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrpPheThrSerTrpSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-701-2002) Cell Biology, Albert Einstein
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
                                                                                                                                                                                                                                                                                                                                      ValAspAspLeuArgAspAlaPheArgThr 195
                                                                                                                                                                                                                                                                                                                                                   /cell_type="hybridoma P1-5"
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/organism="Mus musculus"
/db_xref="taxon:10090"
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/db_xref="taxon:9606"
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Mus musculus clone 5 transgenic
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AWEGLHENSVRLSRQFRRILLDLYFVDDLRDAFRTLGL"
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                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                               Unpublished
2 (bases 1 to 596)
2 (bases 1 to 596)
Martin,A and Schaff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
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              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele-
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin
1 (bass 1 to 596)
Martin, A. and Scharff, M.D.
Somațic hypermutation of the AID transgene in B and non-B
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Matches:
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                                                                     /gene="AID"
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Conservative:
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                                             /gene~"AID"
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AWEGLHENSYRLSGOLRRILLPLYFVDDLRADARTLGL
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AF529825
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                   61 GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGGAGAGGCGTGACAGAGGTACA 120
                                                        Unpublished
2 (bases 1 to 596)
2 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-7UL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
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Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates;
1 (bases 1 to 596)
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165 9 147 41 41 41
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Mortis Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys
                                                                                                                                                                                                                                                                                                                                                                            cells and
                                                                                                                             525
                                                                                                  AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGln 175
                                                                                                                B
                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 597)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in
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172
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Conservative:
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/organism="Cricetulus griseus"
/db_xref="taxon:10029"
/clone="11"
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    .597
    /organism="Homo sapiens"
/db_xref="taxon:9606"

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/transgenic
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                                                                                                                                                                                                                                             AF529851.1 GI:22297289
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172.00
100.00%
100.00%
86.87%
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1. .597
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AF529851
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9
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AF529851
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KEYWORDS
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/product."AID"
/product."AID"
/db_xrefn_id."AAM95442.1"
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GYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVAIJFLRGNPNL
SGLRIFFARLYRCEDRRAEPEGLARLHRAGVOIAIMTRDYFYCWNTFVENHERTFRAW
EGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTWGR"
162 c 148 t
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                                                                                                                                                                                                                                                                                                                                           LeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyrPhe 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 TyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpxlluGlyLou 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeuLeuProLeuTyrGlu 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGlyAsnProAsnLeuSor
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Matches:
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                                                /organism∵"Homo sapiens"
/db_xref∵"taxon:9606"
<1. .591
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'db_xref…"taxon:10029"
                     /cell_line…"CHO'
                                                                                                                                                                                                                                                                                                                       US-09-966-880A-8 (1-198) x AF529855
                                                                                                                   /codon_start::1
                                                                                                                                                                                                                                             4.58e-171
170.00
100.00%
100.00%
85.86%
                                                                                           <1. .591
/gene:"AID"
         /clone-"15"
                                 /transgenic
                                                                                   /gene "AID"
                                           . 591
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Best Local Similarity:
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Sciurognathi; Muridae; Cricetinae;
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USA
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U.
Location/Qualifiers
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Rodentia;
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the
                                                                                              US-09-966-880A-8 (1-198) x AF529825
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                     3.99e-172
171.00
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86.36%
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chinese hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                    Best Local Similarity:
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           ignment Scores:
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/translation="MOSLLMNRRKFLYQFKNVRWAKGRRETYVCYVVKRRDSATSFSL DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCRHVADFLRGNP NUSLBIFFTARLYFCEDRRAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK AWEGHHENSVRLSROLRRLYFVDDLRDAFRTLGL"

163 c 165 g 156 g
                                                                                                                                                                                                                                                                                              AF529835 5YN 19-AUG-2002
Mus musculus clone 8 transgenic Homo sapiens AID (AID) mRNA,
                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus Sukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Makaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 596) Martin, A. and Scharff, M.D. Somatin, A. permutation of the AID transgene in B and non-B cells Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases I to 596)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
                                                                                                                                                               300 GAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAA
                                                                                                                                                160 sAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLe
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Mismatches:
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/db_xref="taxon:10090"
/clone="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .>596
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/db_xref="G1:22297258"
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169.00
98.99%
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/gene="AID"
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AF529835
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Best Local Similarity:
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NLSLARFTARLYFCEDRKAEPBGLERLUHRAGYQIAINFKDYFYCWNTFVENHERTFK
163 c 156 g 150 t
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                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                           e of
USA
                                                                                                               Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B and non-B cells
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
                                                                                                                                                       Organization (17-2002)

Wartin, A. and Scharff, M.D.
Direct Submission (17-301-2002) Cell Biology, Albert Einstein College Submitted (17-301-2002) Cell Biology, Albert Einstein College Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                         /cell_type="hybridoma Pl-5"/transgenic
                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                   1. .596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 596)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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             GI:22297253
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169.00
98.99%
98.99%
85.35%
                                                                                                                                                                                                                                                                                                                                                                                                   /gene="AID"
1. .>596
                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="AID"
                                                                                                                                                                                                                                                                                                                                                                                        .>596
                                                          musculus
                                         house mouse.
Mus musculus
AF529833
AF529833.1
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KAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLR
RILIPLYEVDDLAFRFWGR"
153 c 147 g 135 t
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8 AID (AID) mRNA, partial cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPhe
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Mismatches:
Indels:
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Matches:
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/db_xref."taxon:9606"
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AF529822
                                                               /codon_start~2
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                                                                         /product "AID"
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Query Match:
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16 transgenic Homo sapiens AID (AID) mRNA,
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                                                             AlaLysGlyArgArgGluThrTyrLeu-CysTyrValValLysArgArgAspSerAlaTh 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 547)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martin, A. and Scharff, M.D. Somatic hypermutation of the AID transgene in B cells and non-B
                                                                                                         rSerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLe
                           1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
                                                                        MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp
                                                                                                                                                                                                       pPheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGl
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1. .547
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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1 (bases 1 to
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AF529856
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AMEGLHENSVRLSRQLRRLLLPLYEVDDLRDAFRTLGL"
163 c 151 g 151 t
                                                                                                                          mRNA linear SYN 19-AUG-2002
Homo sapiens AID (AID) mRNA,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                 2 (bases 1 to 595)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                             cells
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  sAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLe
            1 MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in
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1. .>595
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/organism="Mus musculus"
                                                                                                                          AF529834 595 bp
Mus musculus clone 7 transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="hybridoma/transgenic
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149.00
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                                             Unpublished
2 (bases I to 596)
2 (bases I to 596)
4 (bases I to 596)
5 (bases I to 596)
5 (bases I to 596)
8 (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA 1. 596
          Martin, A. and Scharff, M.D. Somatic hypermutation of the AID transgene in B cells and non-B
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Indels:
                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 8"
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                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                             /product="AID"
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160.00
98.99%
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597 bp mRNA linear SYN 19-AUG-2002
13 transgenic Homo sapiens AID (AID) mRNA,
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Rodentia; Sciurognathi; Muridae; Cricetinae;
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and non-B
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Conservative:
Mismatches:
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1 (bases 1 to 597)
Martin,A. and Scharff,M.D.
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Mammalia; Eutheria;
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/protein_id="12297260"
/db_xref="G1:22297260"
/db_xref="G1:2229726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA linear SYN 19-AUG-2002
Homo sapiens AID (AID) mRNA,
                                                                                                                                                                                                      240
                                                                                                                              PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 596)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-1012) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                    /cell_type="hybridoma Pl-5"
/transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .596
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .>596
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/gene="AID"
1. .>596
/gene="AID"
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/translation="MOSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL DFGYLRNKNCHVELLFLYTSDWDLDPGRCYRVTWFTSWSPCYDCRRHVADFLRGNP NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK AWEGLHENSVRLSCRRILLPLYEVDDLRDAFRTLGL"

164 c 154 g 150 t
                                           AF529828 597 bp mRNA linear SYN 19-AUG-2002
Mus musculus clone l transgenic Homo sapiens AID (AID) mRNA,
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Sciurognathi; Muridae; Murinae; Mus.
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                                                                                                                                                non-B cells
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/db_xref="G1:22297244"
                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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/db_xref="taxon:9606"
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/clone="1"
                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                      Martin, A. and Scharff, M.
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                                                                                        GI:22297243
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/db_xref="G1:22297294"
/db_xref="G1:22297294"
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NLSLR1FTARLYFCBDRKAEPEGLRELHRACVQIAIMTFKDYFYYWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLDLYEVDDLRDAFRTWGR"
164 c 156 g 148 t
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/db_xref="taxon:9606"
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                    /organism="Cricetulus /db_xref="taxon:10029" /clone="13"
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Cricetulus griseus clone 1 transgenic Homo sapiens AID (AID) mRNA,
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/db_ref="taxon:10029"
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                           US-09-966-880A-8 (1-198) x AF529824 (1-596)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 597)
Martin,A. and Scharff,M.D.
Direct Submission
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Martin, A. and Scharff, M.
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Mammalia; Eutheria;
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AWEGLHENSVRJRGDRRILLDLYEVDDLRDAFRTLGL"
163 c 156 g 150 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 596)
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10461, USA
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                            SAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArglleLe
              pPheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGl
                                                                    yAsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLy
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                                                                                                                                                                                                                                                             480 AGCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCT
                                                                                                                                                                                                                                                                                      /gene="AID"
/note="integrated into Burkitt's lymphoma cell line
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein (Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY Location/Qualifiers
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Somatic hypermutation of the AID transgene in
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10 AID
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//protein_id="AAM95417.1"

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NLSLATFRLYFCEDRKAEPEGLRRLHRAGYVOIAIMSFKDYFYCWNTFVENHERTFK
AMEGLHENSVRLSRQLRRLLDFLYEVDDLRDAFRTLGL"

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Martin, A. and Scharff, M.D.
Direct Submitted (17-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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164 c 157 g 147 t
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Mus musculus clone 3 transgenic Homo sapiens AID (AID) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                  180
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Matches:
Conservative:
Mismatches:
Indels:
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1. .597
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                                                                                          /codon_start=1
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98.98%
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1. 507
/transgenic
                                                                            /gene="AID"
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Best Local Similarity:
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Cricetulus griseus clone 5 transgenic Homo sapiens AID (AID) mkNA, complete cds. AF529845.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
2 (bases 1 to 597)
2 (bases 1 to 597)
Martin,A and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                       PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly
                                                                                                                                                                                                                                                                                                                                                           AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAluThr
                                                                                                                                                                                         SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeu
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1 (bases 1 to 597)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID
 US-09-966-880A-8 (1-198) x AF529838 (1-596)
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/transgenic
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Mus musculus clone 11 transgenic Homo sapiens AID (AID) mRNA,
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Sciurognathi; Muridae; Murinae; Mus
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Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
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Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
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Martin, A. and Scharff, M.D.
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AF529838.1 GI:22297263
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SYN 19-AUG-2002

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cells

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AWEGLHENSVPLSCARILLPLYEVDDLRDAFRTIGL"
165 c 155 9 149 t
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                                      Euteleostomi;
                                                                                                              2 (bases I to 596)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
                                                                                non - B
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                                                                                cells and
                                     Craniata; Vertebrata; I
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                            /gene="AID"
/note="integrated into Burkitt's lymphoma
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Mismatches:
Indels:
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Matches:
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1. .>596
                                                         1 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID
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                                     Chordata;
                                                Primates;
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64.65%
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1. .>596
                                    Eukaryota; Metazoa;
                                               Mammalia; Eutheria;
                           sapiens
                                                                                                    Unpublished
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Best Local Similarity:
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                                                                                        /protein_id="AAM95432.1"
/da_xxef="01:22297278"
//tanslation="MDSLLMRRKFLYQFKNVRWAKGRRETYLCYVVRRRDSATSFSL
DFGYLRNKNGCHVELFPLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLARFTARLYFCEDRKAEPEGLRRLHRAGYVOIAINWFKDYFYCWNTFVENHERTFK
A 163 0 149 t
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7 AID (AID) mRNA, partial cds.
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/db_xref="taxon:9606"
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AF529821
AF529821.1 GI:22297229
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                                                                   /codon_start=1
/product="AID"
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                          /gene="AID"
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Best Local Similarity:
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596 bp mRNA linear SYN 19 AUG-2002
Mus musculus clone 12 transgenic Homo sapiens AID (AID) mRNA,
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                     non-B cells
1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAATGTCCGCTGG
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B and
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/organisma"Mus musculus"
/db_xrefa"taxon:10090"
/clone:12"
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Rođentia;
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/genec:"AID"
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Mammalia; Eutheria;
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AWEGLHENSVRLSRQLRRILLPLYSVDDLRDAFRTWGR"
164 c 158 g 148 t
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8 transgenic Homo sapiens AID (AID) mRNA,
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                                                            sAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLe 180
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Sciurognathi; Muridae; Cricetinae;
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2 (bases | Lo 597)

Martin,A. and Scharff,M.D.

Direct Submission

Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                            non-B
                        rPheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLy
                                                                          and
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Matches:
Conservative:
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/organism="cricetulus griseus"
/dd_xref="taxon:10029"
/clone="8"
/cell_line="CHO"
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Indels:
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/db_xref="taxon:9606"
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Rodentia;
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Martin, A. and Scharff, M.D.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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complete cds.
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AF529848
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/translation="MDSLLMNRRELYQFKNVRWAKGRETYLCYVVKRRDSATSFSL
DFGYLRNKWGCHVELLFLRYISDWDLDPVRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
WARGLHENSVRLSRQLLELPLYFVDDLRDAFRTWGR"
164 c 156 g 149 t
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Unpublished
2 (bases 1 to 597)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-2012) Cell Biology, Albert Einstein (
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
Medicine, Location/Qualifiers
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/db_xref="GI:22297288"
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/db_xref="taxon:9606"
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/organism="Cricetulus gr/db_rref="taxon:10029"
/clone="10"
/cell_line="CHO"
                              the AID
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                  Martin, A. and Scharff, M.D
Somatic hypermutation of
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Martin, A. and

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Best Local Similarity:
Query Match:
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                                    /translation="MOSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDGRHYADFLRGNP
NUSLRIFTARLYFCEDRRAETBGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
MASGLHENGVRLAETLYFVDDLRDAFRTLGL"
163 c 155 g 150 t
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AID (AID) mRNA,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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10 transgenic Homo sapiens
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197
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                                                                                                                                          Conservative:
Mismatches:
Indels:
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Matches:
                /protein_id="AAM95426.1"
/db_xref="GI:22297266"
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/codon_start=1
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        /product="AID
                                                                                                                      4,74e-120
122.00
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98.99%
61.62%
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AF529850
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AF529850
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596 bp mRNA linear PRI 19-AUG-2002
5 AID (AID) mRNA, partial cds.
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/db_xref="G1:22297226"
/translation="MDSLLMNRRKFLYQFKNVRWAKGRRETY!.CYVVKRHDSATSFSL
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NLSLRIFTARLYFCEDHKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
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Catarrhini; Hominidae: Homo.
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (UT-3002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
non-B
                                                 120 sAlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGln1lcAlallcMctTh
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae: H
1 (bases 1 to 596)
Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B cells
cells
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/db_xref="taxon:9606"
/clone="Ramos 5"
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AF529819
AF529819.1 GI:22297225
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2 (bases 1
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VERSION
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AUTHORS
TITLE
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AF529819
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AUTHORS
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DFGYTRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDHRAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSCRRLLLPLYEVDDL"
163 c 154 g 151 t
                                                                                                                                                                                                 PRI 19-AUG-2002
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4 truncated AID (AID) mRNA, complete cds.
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Catarrhini; Hominidae; Homo.
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USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B cells and non-B
                                                           2 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College Medicine, 1300 Moris Park Ave. Chanin 404, Bronx, NY 10461, U Location/Qualifiers
                                                                                                               596
188
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Matches:
Conservative:
Mismatches:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 4"
1. .596
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/protein_id="AAM95405.1"
/db_xref="GI:22297224"
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AF529818
AF529818.1 GI:22297223
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118.00
98.95%
98.95%
59.60%
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1. .570
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VERSION
KEYWORDS
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AF529818
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TITLE
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/procein_id="AaAM95407.1"
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/brocein_id="AaAM95428"
/translation="MadiLawrenger"/
DEGYLRNKNGCHVELLELRYISDMDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCVDRRAPEGILRRHRAGVOIAIMTFKDYFYCWNTFVENHERTFK
AMGGLHENSYRLSRQLRRLLDFYFVDDLRDAFRTLGI"
164 155 9 151 t
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      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 6"
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                                                                                /product="AID"
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116.00
98.99%
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                                      /gene="AID"
1. .>596
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AF529849
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6 AID (AID) mRNA, partial cds.
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-B
                                                                                      PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly
                                                                                                                                                                                                                                   AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThr
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                                                                                                                                                         SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu
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Catarrhini; Hominidae;
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                      Matches:
Conservative:
Mismatches:
              Length:
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                                                       Gaps:
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Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 596)
Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID
                                                                       (1-596)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens clone Ramos
AF529820
AF529820.1 GI:22297227
                                                                       US-09-966-880A-8 (1-198) x AF529819
             8.45e-116
118.00
98.99%
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Unpublished
                         Percent Similarity:
Best Local Similarity:
Query Match:
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      Scores:
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AUTHORS
TITLE
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AF529820
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REFERENCE
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NSVRLSRQLRRILLDLYEVDDLRDAFRTLGL"
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Mus musculus clone 13 transgenic Homo sapiens AID (AID) mKNA,
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Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B and non-B cells Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2. (bases 1 to 577)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-40L-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
                            241 TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGG
                                                        AsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGlu-AspArgly
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Conservative:
Mismatches:
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<1. .>577
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/codon_start+3
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1. .577
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<1. .>577
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Pred. No.:
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ORIGIN
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TITLE
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AUTHORS
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AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTWGR"
158 g 148 t
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Cricetulus griseus clone 9 transgenic Homo sapiens AID (AID) mRNA,
complete cds.
AF529849
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10461, USA
                                                                                                                           Craniata; Vertebrata; Euteleostomi
Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                non-B
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                                                                                                                                                                                                                                     2 (bases 1 to 597)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-5UL-2002) Cell Biology, Albert Einstein Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
Location/Qualifiers
                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597
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Mismatches:
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Matches:
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/db_xref="taxon:9606"
1. 597
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                                                                                                          Cricetulus griseus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                 1 (bases 1 to 597)
Martin, A. and Scharff, M.D.
                                                                 AF529849.1 GI:22297285
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1. .597
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AUTHORS
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AUTHORS
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AWEGLHENSYRLSRQLRRILLDLYEVDDLRDAFRTLGL"
127 a 165 c 155 g 149 t
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(AID) mRNA, partial
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Matches:
Conservative:
Mismatches:
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13 AID
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AF529827
AF529827.1 GI:22297241
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114.00
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98.99%
57.58%
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Best Local Similarity:
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                                                                                      TyrLeuCysTyrValValLysArgArgAspSerAlaThrSerPheSerLeuAspPheGly
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E 2 (bases 1 to 596)
RATIO.A. and Scharff, M.D.
Direct Submission
AL Submitted (17-JUL-2002) Cell Biology, Albert Einstein Coll
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 104/
Coation/Qualifiers
Location/Qualifiers
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia: Eutheria Primates; Catarrhini; Hominidae;
I (bases 1 to 596)
Martin, A. and Scharff, M. D.
Somatic hypermutation of the AID transgene in B cells
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2 AID (
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AF529816
AF529816.1 GI:22297219
                           US-09-966-880A-8 (1-198) x AF529840
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58.08%
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/db_xrefo...ci:22297296...
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NLSIATEFRELYFCRAFFEBGLERRHARAGYOIAINTFKDYFYCWNTFYENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTWGR...
158 g 148 t
                                                                                                                                                        SYN 19-AUG-2002
AID (AID) mRNA,
                           160 sAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLe 180
   420 CTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGCTTTTCAA 479
                                                                                                                                                                                                                                          Cricetulus griseus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                   College of
10461, USA
                                                                                                                                                                                                                                                                                              1 (bases 1 to 597) Martin,A. and Scharff,M.D. Somatic hypermutation of the AID transgene in B cells and non-B
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                                                     480 AGCCTGGGAAGGCCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCT
                                                                           Unpublished
2 (bases 1 to 597)
Martin, A. and Scharff,M.D.
Direct Submitted (17-JUL-2002) Cell Biology, Albert Einstein (Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
                                                                                                                                         Cricetulus griseus clone 14 transgenic Homo sapiens complete cds.
AF529854.1 GI:22297295
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/db_xref="taxon:10029"
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/db_xref:"taxon:9606"
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DEGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWRTSWSPCYDCARHVADFLRGNP
NLSLRIFIARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
MWEGLHENSVRLZGOFRRILLPLYEVDDLRDAFRTLGL"
163 c 155 g 151 t
                                                                                                                                                                                                                                                                  /note="integrated into Burkitt's lymphoma cell line Ramos"
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  Euteleostomi;
                                                                                  Wartin, A. and Scharff, M.D.
Direct Submission Coll Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                   non-B
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                                                  Somatic hypermutation of the AID transgene in B cells and
Craniata; Vertebrata; Eutelo
Catarrhini; Hominidae; Homo
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 13"
                                                                                                                                                                                                                                                                                                       /protein_id="AAM95414.1"
/db_xref="G1:22297242"
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 Chordata;
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1 (bases 1 to 596)
Martin,A. and Scharff,M.
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Eukaryota; Metazoa;
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Homosapiens AID gene for activation-induced cytidine deaminase, Complete cds.

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Isolation, tissue distribution, and chromosomal localization of the
human activation-induced cytidine deaminase (AID) gene
Genomics 68 (1), 85-88 (2000)
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  AWEGLHENSVRLSROLRRILLPLYEVDDLRDAFRTLGL"
164 c 156 g 148 t
                                                        cytidine deaminase
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AID; activation-induced
Homo sapiens DNA.
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Mammalia; Eutheria;
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADILRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDDFYCWNTFVENHERTFK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
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                                sAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLe
                                                                                                                                                                                                            sAlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"AID"
/protein_id-"AAM95404.1"
/db_xref-"G1:22297222"
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1 (bases 1 to 596)
Martin, A. and Scharff, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Martin,A. and Scharff,M.D.
Direct Submission
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/gene="AID"
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Bukaryota: Matazoa; Chordata; Craniata; Vertebrata; Eutelcostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eukaryota: Maratunga; Catarrhin; Hominidae; Homo.

I (bases I to 7113)

Barbaroks. Lo Amaratunga; H.C., Arej, R.R., Ayele, M. Banks, T., Barbaroks. S. Briewa M., Blanks, T., Barbaroks. S. Briewa M., Brown. E., Boron, M., Bryanin, D., Boude, S., Burkett, C., Burrell, K.L., Byrd, N.C., Catrer, M., Cavazos, S.R., Checko, J., Chowez, D., Coxe, C., Coxe, C., Coxe, C., Coxe, C., Coyle, M.D. Dathorne, S.R., David, R., Debland, C.D., Coxe, C., Coyle, M.D. Dathorne, S.R., Dubnin, H., Devile, D., Dathorne, S.R., David, R., Debland, C.D., Coxe, C., Ople, M.D. Dathorne, S.R., David, R., Debland, C.D., Coxe, C., Ople, M.D. Dathorne, S.R., David, R., Debland, C.D., Coxe, C., Ople, M.D. Dathorne, S.R., David, R., Debland, C.D., Coxe, C., Ople, M.D. Dathorne, S.R., David, R., Debland, C.D., Coxe, C., Ople, M.D. Dathorne, S.R., David, R., Cachardar, C., Eddard, C.D., Eddard, C.D., Eddard, J., Foster, P., Esronto, M., Ealls, T., Ferraguto, D., Elagan, R., Carler, T., Garza, N., Galla, R., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Gavara, W., Gunartone, P., Hale, S., Handes, A., Harnandez, J., Harris, C., Harris, R., Harris, C., Hand, J., Harris, C., Harris, R., Marris, R., Marris, C., Hollins, B., Lee, L., Lowis, L.C., Lee, R., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Liu, J., Liu, M., Loulseged, H., Martin, R., Martin, R., Martindale, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martiney, E., Mocled, R., Pace, A., Martindale, R., Martin, R., Warder, L., Pickens, R., Prickens, R., Prickens, R., Prickens, R., Prickens, R., Morlage, R., Mosch, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Mart
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Direct Submission
Submitted (25-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 71132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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/gene="AID"
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NLSLRFTARLYFCBRAEPGGLRRLHRACYQIAIWFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYFVDDLRDAFRTLGL"

2273 c 2373 g 3253 t
                                                                                                                                                                                                                                                                   Direct Submission
Submitted (18-MAR-2000) Tasuku Honjo, Kyoto University, Department
of Medical Chemistry, Faculty of Medicine; Yoshida, Sakyo-ku,
Kyoto, Kyoto 606-9501, Japan (E-mail:honjo@mfour.med.kyoto-u.ac.jp,
Tel:81-75-753-4371(ex.4711), Fax:81-75-753-4388)
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                                                                                                and Durandy, A. Activation-induced cytidine deaminase (AID) deficiency causes the autosomal recessive form of the Hyper-IgM syndrome (HIGM2) 20460541
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Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.
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113 LeuTyrPheCysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAla 132
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17426. .17575
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/rpt_family="Aluy"
complement(1367)
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12625. 1900
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complement(13980, 14193)
/rpt_family="LIMB5"
14622, 14924
                                                                                                                                                                                                                                                                                          /rpt_family="MIR"
complement(7033. .7327./rpt fac.")
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8567. RAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="MIR"
complement(8815. .9101)
/rpt_family="AluSg"
complement(11227. .12175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name="87432"
/rpt_family="AT_rich"
5305, .5563
/rpt_family="AluJo"
5564. .5599
                                                                              'rpt_family="AT_rich"
644. .5733
                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="FLAM_A"
7980. .8047
                                                                                                                                                                                                                                                                            /rpt_family="(CAA)n"
complement(6711. .68
                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alusx"
7607. 7715
                                                                                                                                                        /rpt_family="AluSq"
6020. .6336
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6630. .6650
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19021. .19314
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                                                                          CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                 STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < le-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
On May 25, 2002 this sequence version replaced gi:20901754 INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1. .1448)
/note="overlaps bases 1. .1448 of clone AC092490"
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/rpt_family="FLAM_C"
5275. .5304
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3296. 3328
/rpt_family="(TTTC)n"
4097. 4249
/rpt_family="Alusq"
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/standard_name="57233"
439. .560
/standard_name="92005"
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1591. .1807
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1966. .2264
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/rpt_family="MIR"
903. 1190
/rpt_family="AluSq"
1191. .1213
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/clone="RP11-438L7"
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1. .71132
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/rpt_family="Aluy"
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AC094826.2 GI:17941606
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Worley, K.C.
                                                                 61 unordered pieces
AC094826
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Rattus norvegicus
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Unpublished
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                                                 DEFINITION
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             RESULT 48
AC094826
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42531 CTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGGGGCTGCACCGCGCC 42590
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Muramatsu,M., Sankaranand,V.S., Anant,S., Sugai,M., Kinoshita,K., Davidson,N.O. and Honjo,T.
Davidson,N.O. and Honjo,T.
a novel member of the RNA-editing deaminase family in germinal center B cells
J. Biol. Chem. 274 (26), 18470-18476 (1999)
                                                                                                                                                                                                                                                                                                                                                   Muramatsu, M. and Honjo, T.
Direct Submission.
Submitted (04-MAR-1999) Medical Chemistry, Kyoto University, Konoe Yoshida Sakyo-ku, Kyoto 606-8501, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 ArgCysTyrArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHis 93
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Indels:
                        /note="APOBEC-1 homologue"
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/organism="Mus musculus"
/db_xref="taxon:10090"
1. .2440
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ACO94826 143044 bp DNA linear HTG 20-DEC-2001
Rattus norvegicus clone CH230-2013, *** SEQUENCING IN PROGRESS ***,
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Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
Submitted (15-SEP-2001) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15624662.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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Center project name: GBMC
Center clone name: CH230-2013
Center clone Namery Statistics
Assembly program: Phrap; version 0.990329First call to
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Web site: http://www.hgsc.bcm.tmc.edu/
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74 ArgCysTyrArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHis 93
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                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
             Consensus quality: 110311 bases at least Q40 Consensus quality: 11877 bases at least Q30 Consensus quality: 125541 bases at least Q20 Estimated insert size: 109318; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation Quality coverage: 1.7x in Q20 bases; sum-of-contigs estimation
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 60 contigs. The true order of the pierrs is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as trus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
     of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 18, 2002 this sequence version replaced g1:20514478.
                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 127845 bases at least Q40 Consensus quality: 134816 bases at least Q30 Consensus quality: 140379 bases at least Q20
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                                                                                                                                                                                                       Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                       Center clone name: CH230-3215
----- Summary Statistics
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Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 177103)
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US-09-966-880A-8 (1-198) x AC120617 (1-177103)

Direction of the solution of t ACL19975 50269 bp DNA linear HTG 02-MAY-2002 Mus musculus clone RP24-483K3, LOW-PASS SEQUENCE SAMPLING. AC119975 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 54 GlyCysHisValGluLeuLeuPheLeuArgTyrIleSerAspTrpAspLeuAspProGly 73 Center: Whitehead Institute/ MIT Center for Genome Research NOTE: This record contains 65 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. Contact: sequence_submissions@genome.wi.mit.edu Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-483K3 Web site: http://www-seg.wi.mit.edu ---- Project Information project name: L25744 Center clone name: 483_K Genome Center Center project name: AC119975.1 GI:20389635 Mammalia; Eutheria; Ro 1 (bases 1 to 50269) Center code: WIBR HTG; HTGS_PHASE0 142422 GTGGCT 142427 Mus musculus. Mus musculus 94 ValAla 95 Unpublished DEFINITION ACCESSION VERSION ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL RESULT 50 AC119975 KEYWORDS COMMENT LOCUS q qq g ò ò

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/db.cref="taxon:10090"
/clone="RP24-483K3"
/clone_lib:"RPCI-24 Male Mouse BAC"
9403 c 9549 g 12707 t 6576 others
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5482: gap of 100 hr
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34756: contig of 644 bp
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      161: gap of 10
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                            quenced to completion. In the event that is updated, the accession number will
However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                       685 784: gap of 100 bp
785 1439: contig of 655 bp in length
1440 1539: gap of 100 bp
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20879: contig of 683 bp in length
20979: gap of 100 bp
21667: contig of 688 bp in length
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of 100 bp
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13865: contig of 660 bp in length
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14653: contig of 688 bp in length
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17754: contig of 683 bp in length
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20096: contig of 679 bp in length
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23974: contig of 677 bp in length
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in length 50269 38 0

in length

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
    Submitted (03-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                  Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 98161)
Worley, K.C.
Direct Submission
Submitted (13-UUL-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this Sequence version replaced gi:18860460.
                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 54904 bases at least Q40
Consensus quality: 57914 bases at least Q30
Consensus quality: 60850 bases at least Q30
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Alstrongs 5 L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbard, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bunkert, C., Burch, P., Burkett, C., Burch, P., Burkett, C., Burch, P., Burkett, C., Burch, P., Burkett, C., Burch, J., Chavez, D., Carron, T.E., Carrer, M., Cavazos, S.R., Clacko, J., Chavez, D., Carron, T.E., Chen, Z., Chowdhy, I., Christopoulos, C., Clen, G., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David,
                                                                                                                                                                                                                                                                                     Ratius norvegicus clone CH230-98A4, *** SEQUENCING IN PROGRESS ***, AC109119
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                     58 GluLeuLeuPheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCysTyrArg
                                                                                                                                                                                                                     78 ValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHisValAla 95
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    Mismatches:
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Best Local Similarity: 100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                Mus musculus clone RP24-483K3, LOW-PASS SEQUENCE SAMPLING.
AC119975
AC119975 GI:20389635
MIST HTGS_PHASED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wl.mit.edu
------ project Information
Center project name: L2574
                                                                                    4318 cGGTGTTACCGTGTCACCTGGTTCACTTCCTGGAGCCCCTGC 4277
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                                                   74 ArgCysTyrArgValThrTrpPheThrSerTrpSerProCys
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/db_xref="taxon:10090"
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Metzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C.,
Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T.,
Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T.,
Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J.,
Buhay,C., Burac,C., Burkett,C., Checko,J., Chen,G.,
Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S.,
Fernandez,C., Ferragutc,D., Forcum-Tansey,J., Gill,R.,
Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M.,
Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Nassey,E., McLeod,M.P., Mel,G., Moore,S., Morgan,M., Martin,R.,
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Wullidamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
Wally,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G.,
Worley,K. and Gibbs,R.
                                                                                                                            AC068309 67244 bp DNA linear HTG 16-OCT-2001 Mus musculus chromosome 13 clone RP23-298J20, *** SEQUENCING IN PROGRESS ***, 22 unordered pieces.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "vorking draft" sequence. It currently

* consists of 22 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley K.C.

Direct Submission

Submitted (12-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 14, 2001 this Sequence version replaced gi:11094637.

Center: Baylor College of Medicine
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                           Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Lof 57244)

1 (Dases 1 to 67244)
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                      26 GluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThrSer 41
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4943: gap of unknown length
9846: contig of 4903 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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AC068309.3 GI:16118088
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.

[Aphydroidea; Drosophila.

[Abases 1 to 7750)

Barrio, R., Shea, M.J., Carulli, J., Lipkow, K., Gaul, U., Frommer, G., Schuh, R., Jackle, H. and Kafatos, F.C.

The spalt-related gene of Drosophila melanogaster is a member of an ancient gene family, defined by the adjacent, region-specific homeotic gene spalt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGOVOGEOTP TRLPFAPPVAPYGOEOHONOVERPEEITPYPOABDLSKRWYKEREKSHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLAKELDADSNNNGTEPQMEAEAVPESDTERETAEERGEEQEPENSNEALDLSIISSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIFATGLANGATGGGSGUGGLPMLGMPMPNILLMAAAREEMHALGHAHAKFFILPFG
PLGFWGLHPPPNVCNLCFKMLPSLAALESHLQSEHAKEPATGHAQRPHCSDAGSBYGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDHESRREENSKTDKRGTEDRKAEPEGYQSMMCDISSSLASSITNHDPPPAPNEPNC
LEMLQRRTEEVLDSASQSLHAAQMQEEYSEYASKEAQSRGEIFKHRCKYCGKIFGSYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVNNKHFCHVCRRNFSSSSALQIHMRTHTGDKPFQCNVCQKAFTTKGNLKVHMGTHMM
INPTSRRGRRMSLELPMRPGPNSGQGHPGSSAEQEFMQRRPELFFPYLPPFFNGLPPK
                                                                                                                                                                                                                                                               Direct Submission
Submitted (26-AUG-1996) R. Barrio, European Molecular Biology
Laboratory, Meyerhofstrasse 1, Heidelberg, D-69117 Heidelberg, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"MCSIFRNRINYRGTGGTRSGSGERERDRDRDRDRDRDRERDRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGEGSGTGATSNYPQEAGDAEQSLMKMQLHAHRFPASPLDFQQALMSAGPPTSSLDP
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JOURNAL
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AUTHORS
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plasmid AT, section 46 of 50 of
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Agrobacterium tumefaciens str. C58 (Cereon)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 10945)
HinkLe,G., Slater,S.C. and Goodner,B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall Disease in Plants
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Matches:
Conservative:
Mismatches:
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Agrobacterium tumefaciens str. C58
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9.00
100.00%
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1 1894 c
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Query Match:
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ORIGIN
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                                                                                                                                                                                                                                                                                 VAKLAILDGVPILEALEHCNARFATQWWHWFFFAQHDKPEQAISADPLRWYGGTEDLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAHDASRISRATKALSHAVGNLOTRYSLSSAKCDAVTRALORFNAAWAEYSSRFVLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HKASAANATASDVQALRRKVADLSYRMQQLEDDVADNAALRGEVIRMRREIAITQSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation⇔"MPRSKLKLVSLTPLFAALAASPLVQQTVAATA1VSLSMGQAVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPVRMNAPALLGDMRRSLAEIAFSFSEAKGDSKRRSGVAVLAALTEATQAVQSLETAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="conserved hypothetical protein - Deinococcus
- Deinococcus radiodurans (strain R1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDTLPSSENSDEPRAGMRVQEDKASEEEPVMKATP<sup>1</sup>
3145 c 3105 g 2388 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(850]. .9256)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="AGR_pAT_745"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(7724. .8416)
/genen"AGR_pAT_742"
complement(7724. .8416)
/geneu"AGR_pAT_742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(8501, .9256)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start~1
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us-09-966-880a-8.100align.rge

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IFFDHTAGDSFDSSLIDADTAVALLLHDLDLEMPILGAALVATPFYIGALGSSRTHEK
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NSGRKLQCPLRVLWSLRDDLEDLYNDVLAIWQPWAELPVSGLGIDSGHHMAEEAPLEV
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LPFAGRSTYRKVRDRASYAFALVSVAAALDVDDAGNVKDVRLALGGVAHKPWRALKAE
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VLNALFGIYSIPEGPEWRDRAHRIVRLVMDGLRR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="oxidoreductase with iron-sulfur subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="transcriptional
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                                                                                                                                                                                                                                                                     complement(1636. .2220)
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3560. .4093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4090. .5079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Wood, D.W., Setubal, J.C., Kaul, R., Okura, V.K., Almeida Jr., N.F., Chon, Y., Bovee Sr., D., Chapman, P., Clendenning, J., Deatherage, G., Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M., McClelland, E., Palmieri, A., Raymond, C., Rouse, G., Saenphimmachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I., Karp, P., Romero, P., Zhaog, S., Yoo, H., Tao, Y., Biddle, P., Jung, M., Krespan, W., Perry, M., Gordon, E., Eisen, J.A., Biddle, P., Jung, M., Krespan, W., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.

The genome of the natural genetic engineer Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chases 1 to 11013)
Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E.,
Chen, Y., Woo, L., Kitajima, J.P., Okura, V.K., Almeida Jr., N.F.,
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Saenphimmachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I.,
Krapp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M.,
Krespan, W., Perry, M., Gordon, Kamm, B., Liao, L., Kim, S., Hendrick, C.,
Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                     BCT 20-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           C58 AT plasmid section 45 of 49 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens str. C58 (U. Washington).
Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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1. .11013
/organism="Agrobacterium tumefaciens str. C58
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                                                Matches:
Conservative:
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                                                                                                         Mismatches:
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Science 294 (5550), 2317-2323 (2001)
21608550
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Gaps:
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                                                                                                                                                                                                                                                                     125 GlyLeuArgArgLeuHisArgAlaGly 133
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538. .1398
                                                                                                                                                                                                                                                                                                                                                                                                                               11013 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens str.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the complete sequence.
AE008970 AE008687
AE008970.1 GI:17743952
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                      72.4
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and Nester, E.W.
                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                  AE008970
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                                                                         Percent Similarity:
Alignment Scores:
                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                            RESULT 56
AE008970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
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MEDLINE
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CDS

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CE 2 (bases 1 to 59915)

Birten, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boquslavkiy, L., Boukhgallter, B., Brown, A., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Farreira, P., FitzHugh, W., Gage, D., Calagan, J., Gardynus, S., Glodete, M., Graham, L., Grand-Plerre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kells, C., LaRocque, K., Landazares, R., Landers, T., Lehoczky, J., Levine, R., Machen, E., Mihova, T., Macdonald, P., Major, J., Marquis, N., Mathlews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Liu, G., McCarthy, M., McEwan, P., McKernan, K., McPhy, T., Naylor, J., Nquyon, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R. Riebeck, M., Sahcos, R., Schauer, S., Schupbuck, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Subramanian, A., Taslamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Nyman, D., Ye, W. J., Younq, G., Submisted, Submisted, Calmer, A., and Zody, M., Submisted, Calmer, A., and Cody, M., Submisted, Calmer, A., and Cody, M., Submisted, Calmer, A., and Calmer, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACLUUY84 59915 bp DNA linear HTG 23-NOV-2001
Mus musculus clone RP23-76J21, LOW-PASS SEQUENCE SAMPLING.
AC100984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-NOV-2001) Whitehead Institute/MIT Center
Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-76J21
   00000
                                 Conservative:
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                                                                          Mismatches:
   Matches:
                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                   US-09-966-880A-8 (1-198) x AE008970 (1-11013)
                                                                                                                                                    Gaps:
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Center clone name: 76_J_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- Genome Center
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9.00
100.00%
100.00%
4.55%
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HTG; HTGS_PHASE0.
Mus musculus.
Mus musculus
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                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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TITLE
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SOURCE
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SWNGEROTPEDDGFFWSEPRDIRGFKKIATYONGDIAAARYHFGNGIVVLTGPHPEA
GGSWFHEAGIIDKMPDHRVLRSVMDEFRSEPR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTLHNSCPEQFTFPARHLYAAKTFHIGOVADMDMLANTFMRAPGESVGTFALECALD
ELAEKLGLOPPELRRRREPEROPTGRFSSRYLIEAFERGADEGGGGGGTATRORE
EGENILIGMGGATATYPPHRPEGGANER KLTVDGRVTVSTAVHDNGGGGTATAQNGHLAA
RLGLPLDHVTFEYGDSKLPRGVIAGGSTQTASIGGAVIAATFVLVEELIKLSGNDSPL
AGGSLLLEVARARGGGLSHISNSLFESYGSILRRAGREELVCKERAPAFABRAFS
YGAGPCEVHVSARGGETRVSRFLGSFDAGGLINSKMATSOFKGGI INGIGLATFETH
PDERTGRIVNASLADYHVPVQMDVPALEILYTNKPDPQAPMGARGIGEIGITGVGGAV
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PVILPRSLNGAVWRLEGDVGARQIIETSGLRIDVEIGDSAHLDVDTPEAVVAAGGIL
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KAPSLAMASSPTAAGASNLPVMQSDEIHWNGQPIALVLAETQEQADHAASLVTAKYELL
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HAATVVWKDDELRVHDASQLLDLTTGQLADIFGLDVSKVHVTSPYVGGGFGGKCFWDH
QILACAAARLAGRPVRIMLSREGVFRIIGGRTVTEQRVALGAKADGTLDALIHTGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANAVYNATGVRVRDLPITLDKLTGGLD"
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                                                                                                                                                                                                                      /transl_table=11
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However, it should not be assumed that this clone

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Alignment Scores: Pred. No.:

gene

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ed to completion. In the pedated, the accession nup by: contig of 695 bp in 94: contig of 699 bp in 94: contig of 699 bp in 94: contig of 699 bp in 94: contig of 707 bp in 95: contig of 708 bp in 95	27450: contig of 6 550: gap of 10 28255: contig of 7 355: gap of 10

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Direct Submission

Direct Submission

Submitted (05-Jaw-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Birnon, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boquslavkiy, L., Boukhdaller, B., Campopiano, A., Chang, J., Chazaro, B., Grode, P., Dearellano, K., Deark, K., Chark, K., Cook, A., Cooke, P., Dearellano, K., Deark, K., Cook, A., Graham, L., Graham, J., Gardyna, S., Gorde, S., Gorder, M., Graham, L., Graham, L., Gand-Pleire, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McCarthy, M., McEwan, P., McKernan, R., Marquis, N., Matherin, J., Marquis, N., Matherin, J., Naudonald, P., Mafor, J., Marquis, N., Matherin, J., Naudon, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Connor, T., O'Donnell, P., O'Neil, D., O'Liver, J., Peterson, K., Phurkhang, P., Pierre, N., Pothawan, C., Severy, P., Spencer, B., Schueuer, S., Schueuer, S., Schueuer, S., Severy, P., Spencer, B., Tragla, R., No, A., Wilson, B., Wy, Wyman, D., Ye, W.J., Yound, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
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Direct Submission

Direct Submission

Direct Submission

Submitted (08-SEP-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 141899)

Birnen, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dakrellano, K., Dawar, K., Diaz, J.S., Dodge, S., Faro, S., Gorde, S., Gorde, S., Gorde, S., Gorder, J., Gardyna, S., Ginde, S., Gorde, S., Gorder, M., Galagan, J., Gardyna, S., Ginde, S., Gorde, S., Gorder, M., Horton, L., Hulme, W., 111ev, I., Johnson, R., Jones, C., Ramat, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., Maccan, P., McKernan, K., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Maldrim, J., McRamn, P., McKernan, K., McPheeters, R., Maldrim, J., Norbu, C., Norman, C., Phunkhang, P., Plerre, N., Pollara, V., Norbu, C., Norman, C., Phunkhang, P., Plerre, N., Pollara, V., Sancos, R., Suberamanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, N., Viel, R., Vo, A., Wilson, B., Viel, Y., Volan, V., Viel, R., Volan, V., Viel, V., Vie
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Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, Paro, S., Ferreira, P., Filtzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
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Submitted (30-NOV-2001) Whitehead Institute/MIT Center for Genome
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Homo sapiens chromosome 15, clone RP11-814P5, complete sequence.
ACO87457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases I to 141899)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastlen,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                      ACO14357 103746 bp DNA linear HTG 16-NOV-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was identified as CDM:10212654 by the submitter.

For further information on this sequence e-mail to fly@celera.com.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 141899)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chonosome 15, clone RP11-814P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidaa; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103746
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/db_xref="taxon:7227"
21798 c 21974 g 30127 t
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Conservative:
       Mismatches:
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                                                                                                                                        US-09-966-880A-8 (1-198) x AC100984 (1-59915)
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Drosophila melanogaster
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AC014357
AC014357.1 GI:6436978
HTG; HTGS_PHASE2.
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   Best Local Similarity: 100.00%
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KEYWORDS
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Rattus norvegicus clone CH230-137M23, *** SEQUENCING IN PROGRESS AC12306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M. Banks, T., Barton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                             11447. 11452

/notce="<30 qual SNGL region"

1457. 11461

/note="<30 qual SNGL region"

complement(11728. 11816)

/rbt_family="MIR3"

complement(11822. 12123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Alusx"
12056. .12061
//note="<30 qual SNGL region"
12129. .12136
//note="<30 qual SNGL region"
12168. .12174
//note="<30 qual SNGL region"
                                                                                                                                                                                                                                                                                                                                 complement(11110. 11325)
/rpt_family="LIME"
complement(11327. 11603)
/rpt_family="AluJo"
11447. 11452
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Matches:
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                                                                                                                                                                                                                      /rpt_family="MIR"
9570 .9603
/rpt_family="(CAT)n"
9729 .9756
/rpt_family="(CAAAAA)n"
complement(10861 .10957)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC123206.2 GI:21671690
HTG; HTGS_PHASE1.
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100.00%
4.55%
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Mammalia; Eutheria;
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Best Local Similarity:
Query Match:
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AC123206
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AUTHORS
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KEYWORDS
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                                                                                                                  submitted
                                                                                                             Only the first 141.9 kilobases of this clone are being submitted. The remainder overlaps accession number AC018868.
                   Research, 320 Charles Street, Cambridge, MA 02141, USA ON NOV 30, 2001 this sequence version replaced gi:15528911. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@denome.wi.mit.edu
------- Project Information
Center project name: L11876
                                                                                                                                                                                                                                                                                                                                                                                                                            1. .15
//note="<30 qual single clone coverage"
30. .35
//note="<30 qual single clone coverage"
293. .298
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/note="<30 qual single clone coverage"
                                                                                                                                                                                                                                                                                                                                                                              /clone="RP11-814P5"
/clone_lib="RPCI-11 Human Male BAC"
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412. .416
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/note="<30 qual SNGL region"
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382. .396
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/note="<30 qual SNGL region"
1021. .1530
                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
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complement(1726. 2118)
/rpt_family="MER57A"
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239. .6415
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/rpt_family="L2"
2770. .3093
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7570. 7782
/rpt_family="MIR"
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'944. RA'?
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/rpt_family="MLT1K"
complement(8841. .9063)
/rpt_family="MIR"
                                                                                                                                                                                                                                                    Center clone name: 814_P_5
                                                                                                                                                                                                                                                                                    Location/Qualifiers
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317. .3612
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440. .7484
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NOTE: This is a "working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary, caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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On Jul 2, 2002 this sequence version replaced gi:21239988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 150147)
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Sequenciary vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 8848 bases at least 040
Consensus quality: 93252 bases at least 040
Consensus quality: 97242 bases at least 030
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quadilty data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORNEEP: Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                this
this
                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/MEP/Chr6
RP11-400P17 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone SRP11-400P17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-400P17 is at 154288 in this sequence. The true left end of clone RP11-69H11 is at 28928 in this sequence. The true right end of clone RP11-69H11 is at 2000 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8428. .8724
/notbar repeat: matches 1. .296 of consensus"
8725. .8760
/note="L1MB6 repeat: matches 5136. .5170 of consensus"
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8428. .8724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11.2"
543. .849
//octe="Aluy repeat: matches 1. .311 of consensus"
//octe="12.repeat: matches 2610. .2750 of consensus"
//octe="L2_repeat: matches 2610. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"MIR repeat: matches 80. .235 of consensus" 720. .4776

note-"MIR repeat: matches 165. .221 of consensus" 767. .4826

note-"MIR repeat: matches 195. .257 of consensus"
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// Alusx repeat: matches 1. .303 of consensus
/946. .8427
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4344. .4551
/note="MIR repeat: matches 20. .241 of consensus"
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1. .154288
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="MIR re
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/note="L2 re
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Human DNA sequence from clone RPI1-400P17 on chromosome 6, complete
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Submitted (26-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jun 27, 2001 this sequence version replaced gi:14268219.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
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/ucte="AluCe repeat: matches 1. 300 of consensus" 12765. 112905 / 102905 / 112905 / 112905 / 112905 / 112905 / 112905 / 112905 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 112901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12901 / 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L2 repeat: matches 2579. .2604 of consensus"
.2466. .12764
                          /note="AluSq repeat: matches 1. 306 of consensus" 8068. 9174 / note="LiMB6 repeat: matches 5170. 5305 of consens 9193. 9350
                                                                                                                                                      .43 of consensus"
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28120. .28430
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note="7" copies 4 mer tgtg 100% conserved"
2233. .22514
note="AluY repeat: matches 1. .282 of consensus"
2525. .22575
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9353. .9969
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AC113662 158016 bp DNA Linear HTG 13-JUL-2002
Rattus norvegicus clone CH230-15401, *** SEQUENCING IN PROGRESS
***, 56 unordered pieces.
AC113662
AC113662.3 GI:21743470
HTG; HTGS_PHASE1.
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Rodentia; Sclurognathi; Muridae; Murinue;
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.K., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Bunks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bunay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carren, T. Carter, M., Cavazos, S.R., Chacko, J., Clavor, D., Chen, G., Chen, R., Chewland, C.D., Cox, C., Coyle, W.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Alusx repeat: matches 1. .312 of consensus"
33511. .33615
/note-"U6 repeat: matches 3. .107 of consensus"
33631. .34127
/note-"Alusx repeat: matches 1. .295 of consensus"
3462. .3423
/note-"Mar repeat: matches 159. .247 of consensus"
34222. .34281
/note-"L2 repeat: matches 2692. .2747 of consensus"
34551. .34636
/note-"Alusx repeat: matches 2. .297 of consensus"
34559. .35034
/note-"Repeat: matches 2. .297 of consensus"
34550. .35034
                                                                                                                             // 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13164 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 13163 / 131
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/noter"RIR repeat: matches 112. .254 of consensus" 35421. .35662

/noter"AluJo repeat: matches 57. .300 of consensus" 35663. .35692

/noter"AluJo repeat: matches 57. .300 of consensus" 35663. .35692

35772. .36094
                                                                                              .275 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                               /noten"AluSg repeat: matches 1. .301 of consonsus"
32866. .33173
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Mismatches:
Indels:
note"L2 repeat: matches 2663.
30584, .30857
noter"AluJo repeat: matches 1.
10892. .31125
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Mammalia; Eutheria;
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Rattus norvegicus
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
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Wulliams, G., Williamson, A., Wuleczyk, R., Wooden, S., Worley, K.,
Wulliams, G., Wulliamson, A., Wuleczyk, R., Wooden, S., Worley, R.,
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* (See http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 56 contigs. The true order of the pieces

* is not known and thair order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 158016)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-JUL-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 13, 2002 this sequence version replaced g1:19525824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 116208 bases at least Q40
Consensus quality: 119847 bases at least Q30
Consensus quality: 122552 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: GRUR
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Direct Submission
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Stren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastlan, V., Beda, F., Boguslavkiy, L., Baldwin, J., Barna, N., Bastlan, V., Beda, F., Boguslavkiy, L., Baldwin, J., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Callymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Derrette, M., Graham, L., Gradran, S., Ginde, S., Goyette, M., Graham, L., Gradran, S., Ginde, S., Goyette, M., Graham, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Kartus, A., Klein, J., Lanccque, K., Landes, R., Janes, C., Kann, L., Kartus, A., Klein, J., Lanccque, K., Landes, R., Janes, C., Mang, J., Marquis, N., McZarthy, M., McEwan, P., McGurk, A., McKernan, K., McPiveters, R., Marquis, J., Marquis, J., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Livar, T., Raymond, C., Rlaymon, C., Rlaymon, C., Roymon, C., Raymond, C., Rlaymon, C., Roymon, R., Pierre, N., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Triquillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Yeung, G., Zainoun, J., Zimmer, A. and Zody, M., Control, M., Control, M., Control, M., Chan, A., Chan, M., Control, M., Control,
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Barna,N., Bartien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M., Collins,S., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Gage,D.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176053)
On Feb 21, 2001 this sequence version replaced gi:11071943.
Location/Qualifiers
1. .173509
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Mismatches:
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/clone="RP11-627G1"
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                                                                                        /organism~"Homo sapiens"
/db_xref="taxon:9606"
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Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W.,
Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacCean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M.,
McWan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, O., Norbu, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Noil, D., Oliver, J.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Stange-Thomann, N.,
Stoyanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Travers, M., Trayis, N., Yeighio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Direct Submission
Submitted (24-Aug-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 8, 2000 this sequence version replaced gi:7670233.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 19915

Center clone name: 19915

Center clone name: 19915

Sequencing vector: M13: M77815; 100% of reads

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap: version 0.960731

Consensus quality: 170544 bases at least 040

Consensus quality: 17410 bases at least 030

Consensus quality: 174372 bases at least 020

Insert size: 176000; agarose-fp

Insert size: 175153; sum-of-contigs

Quality coverage: 5.0 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ap of 100 bp contig of 30819 bp in length
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1362 1461: gap of 100 bp
1462 4481: contig of 3020 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4482 4581: gap of 100 bp
4582 12932: contig of 8351 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139441 139540: gap of 100 bp
139541 176053: contig of 36513 b
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .08522 108621: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39941 40040: gap of
40041 60017: cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139440:
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60018 60117
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JOURNAL
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AC127421 179510 bp DNA linear HTG 17-JUL-2002 Mus musculus chromosome UNK clone RP24-314F1, WORKING DRAFT SEQUENCE, 8 unordered pieces.
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Submitted (17-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 179510)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (15-JUL-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 179510)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              905 others
                /clone_lib="RPCI-11 Human Male BAC" 1. .1361
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Matches:
Conservative:
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| 37507 c 38347 g 50081 t
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                                                                                                                                                                                                                                  27404. .39940
/note="assembly_fragment"
40041. .60017
/note="assembly_fragment"
60118. .83591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of Mus musculus clone Unpublished
                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
83692. .108521
/note="assembly_fragment"
108622. .139440
                                                                                                                                                                                                                                                                                                                                                                                       108622. .139440
/note="assembly_fragment"
                                                                          462. .4481
'note="assembly_fragment"
                                                                                                               4582. 12932
/note="assembly_fragment"
13033. 27303
/note="assembly_fragment
                                                          'note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 179510) McPherson,J.D. and Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 AlaThrSerPheSerLeuAspPheGly 47
/clone="RP11-419E16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                             vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                 .176053
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AC127421.1 GI:21759528
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100.00%
4.55%
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                                                                            1462.
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
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Genome Center

/organism="Homo sapiens" /db_xref="taxon:9606"

source

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contig of 136 bp in length
gap of unknown length
contig of 261 bp in length
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                                                                            63336 AACCTCTCTCTTCGGATATTTACTGCT 63362
       US-09-966-880A-8 (1-198) x AC127421 (1-179510)
                                                    103 AsnLeuSerLeuArgIlePheThrAla 111
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 180668)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                         AC020857.2 GI:6980198
HTG; HTGS_PHASE0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                    ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
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REFERENCE
                                                                                                                                            RESULT 66
                                                                                                                                                                                                                                                                              KEYWORDS
SOURCE
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                                                                                                                                                                 AC020857
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                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * Tuns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  719 others
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gap of unknown length
contig of 49725 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 23449 bp in length
unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 37397 bp in length
unknown length
                                                                                                                                                        Sequencing vector: M13; 0%
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 181162 bases at least Q40
Consensus quality: 182185 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
of 6287 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
of 2751 bp in length
                                             Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 1378 bp in length
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/note="assembly_name:Contig22"
55495. .92891 /
/note="assembly_name:Contig23"
92992. .129685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
Conservative:
Mismatches:
Indels:
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1479. 4229
'notes"assembly_name:Contig18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4330, 10616
/note="assembly_name:Contig20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0717. .34165
note="assembly_name:Contig21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig25"
37702 c 36620 g 52806 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .179510
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/db_xref="taxon:10090"
/chromosome="UNK"
                                                                                                                  Center project name: M_BB0314F01
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Best Local Similarity:
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L Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA ON Feb 16, 2000 this sequence version replaced gi:6686451.

* NOTE: This record contains 205 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful ion

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ACU20857 180668 bp DNA linear HTG 16-
Mus musculus clone RP23-163F21, LOW-PASS SEQUENCE SAMPLING.
ACU20857
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of 1010 bp in length
unknown length
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1094: contig of 298 bp in length
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unknown length
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gap of unknown length
3673: contry of 632 bp in le
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unknown length
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unknown lengt
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39949: contig of 1075 bp in length gap of unknown length 40342 contig of 393 bp in length gap of unknown length app of unknown length app of unknown length gap of unknown length

* 38875	* 39950	* 40343	* 40574 *	* 41329 *	* 41806	* 42226	* 42416	* * 42508	* 42872	* 43645	* 4 43884	* * *	)	* * * * * * * * * * * * * * * * * * *	* 46768	* 47743 *	* 48098 *	* 48245	* 48518	* 49915	* 50068	* 50259	* 4	\$1716 *	* 51715	* 53055	* 53362	* 53542 *	* 53730	* 53992	* 54142	* *	*******	Alignment Scores:	Score:	Percent Similarity: Best Local Similarity:	Query Match: DB:	US-09-966-880A-8 (1-198)
unknown length of 1153 bp in length	unknown length of 721 bp in length	unknown length of 175 bp in length	unknown length of 989 hp in length	unknown is in the state of 940 ha in in landth	unknown length	or you by in religion unknown length of so, he in longth	unknown length	oi 235 bp in length unknown length	of 225 bp in length unknown length	of 108 bp in length unknown length	of 313 bp in length unknown length	of 987 bp in length	orknown longth	589 bp in length	unknown Length of 937 bp in length	unknown length of 1322 bp in length	unknown length of 724 bp in length	unknown length.	unknown length	unknown length		of 1141 bp in length unknown length	of 1034 bp in length	onknown rength of 239 bp in length	unknown length of 240 bp in length		unknown length of 1505 bp in length	unknown length of 1700 bp in length			or 1092 bp in length unknown length	of 158 bp in length	of 682 bp in length	unknown tength	unknown rengin of 164 bp in length	unknown length of 1216 bp in length	unknown length of 302 bp in length	unknown length of 861 bp in length unknown length
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12836:			14721						••		17849:	18836:	19768:	20357:	21294:	22616:						26859:	27893:	28132:	28372:	28958:	30463:	32163:				34584:	35266:	36331:	36495:	37711:	38013:	38874:
* 11684	* 12837	* * 13558	* 13733	* 14722	* 15713	4 *	n 0	6969T *	* 1/204	* 17429 *	* 17537 *	* 17850 *	* 18837 *	* 19769	* 20358	* * 21295	* 22617	* *	T# 500 * *	OTC52 *	* 24821 *	* 25719 *	* 26860	27894	* 28133	* 28373	* * 28959	* 30464	* 32164	* 1	* 53333	* 34427	* 34585	* 35267	* 36332	* 36496	* 37712	38014

48097: contig of 355 bp in length gap of unknown length

-8 (1-198) x AC020857 (1-180668)

9 0 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

9.00 100.00% 100.00% 4.55%

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Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send cmail to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188136 bp DNA linear HTG 17-JUL-2002 Danio rerio clone DKEY-224J12, *** SEQUENCING IN PRUGRESS ***, 10 AL840638
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farlan,D., Feriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostlin,D., Howland,T.J., Ibegwan,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrati,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunco,J., Pacleb,J., Paragas,V., Park,S., Patel,S., Pfelffer,B., Strong,R., Sitpleton, Strong,R., Svirskas,R., Tector,C., Milliams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C. Sequencing of Drosophila chromosome 2L, region 33A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-MAR-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Mar 17, 2001 this sequence version replaced g1:7264773.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley, National Laboratory, MS 64-121
                                                                                                                                                                                                                                                       "Celniker,S.E., Adbayani,A., Arcaina,T.T., Baxter,E., Blaze),R.G., Butanhoff,C., Champe,M., Clavez,C., Chew,M., Ciesiolka,L., Boyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon, Sethl,H., Snir,S., Pfeiffer,B., Poon,L., Sequeira,A., Schli,H., Snir,E., and Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cione_lib."RPC1-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6)"
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/organism."Drosophila melanogaster"
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Matches:
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/clone="BACR43K24 (D575)"
/clone_lib="RPCI-98 (Roswe
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/db_xref="taxon:7227"
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HTG: HTGS_PHASE1.
Danio rerio.
Danio rerio.
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JOURNAL
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AL840638
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KEYWORDS
SOURCE
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                                                                                       Homo sapiens genomic DNA, chromosome 11q clone:RP11-661121, complete sequence. APO03402. APO03402. GI:16751506 HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-MAR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suebiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Nov 5, 2001 this sequence version replaced gi:13366105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
Eukaryota; Metazoa: Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Metazoa: Arthropoda; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila.

1 (bases 1 to 188067)
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INV 17-MAR-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACUU7U83 188067 bp DNA linear INV 17-MAR-
Drosophila melanogaster, chromosome 2L; region 33A-, BAC clone
BACK43X4, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA Published Only in Database (2001)
2 (bases 1 to 187948)
2 (bases 1 to 187948)
2 Lattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                          146416 AACCTCTCTCTTCGGATATTTACTGCT 146442
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Matches:
                                                                                                                                                                                                                                                                                  Homo sapiens DNA, clone:RP11-661121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
  103 AsnLeuSerLeuArgIlePheThrAla 111
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/clone="RP11-661121"
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AC007083.11 GI:13374638
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Best Local Similarity:
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SOURCE
ORGANISM
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DEFINITION
                                                                                                                  AP003402/c
                                                                                                                                                             DEFINITION
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VERSION
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AUTHORS
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                                                                                              RESULT 67
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FEATURES
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AC036188
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                                                                                    Burton,J.

Burton,J.

Submission

Submitted (14-Jul-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CBIO 15A, UK. E-mail enquiries: zface@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

On Jul 19, 2002 this sequence version replaced gi:21748404.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Scrinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 188136)
                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator: 100% of reads Consensus quality: 181961 bases at least Q40 Consensus quality: 184055 bases at least Q30 Consensus quality: 18551 bases at least Q20 Insert size: 18736; sum-of-contigs of Insert size: 157949; 24.5% error; agarose-fp Quality coverage: 12.05x in Q20 bases; sum-of-contigs Quality coverage: 14.71x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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165042 165141: gap of 100 bp
165142 188136: contig of 22995 bp in length.
Location/Qualifiers
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contig of 52487 bp in length
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159423 161843: contig of 2421 bp in length
161844 161943: gap of 100 bp
161944 165041: contig of 3098 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156005 156104: gap of 100 bp
156105 159322: contig of 3218 bp in length
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7005. .13025

fragment_chain:1"

13126. .64622

700te="assembly_fragment:00273

fragment_chain:1"

64723. .73250
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/note="assembly_fragment:02919
fragment_chain:1"
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5065. .13025
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                                                                                                                                                                                                                                                                                                                                             Center project name: zK224J12
                                                                                                                                                                                                                                                                            Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zface@sanger.ac.uk
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/db_xref="taxon:7955"
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                                                                                                                 TITLE
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                                                                                              AUTHORS
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhalater, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kan, L., Karatas, A., Klein, J., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McZarthy, M., McEwan, P., McGurk, A., McMercaran, K., Merbeeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mleng, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T.M., Ollver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymon, C., Schery, P., Spencer, B., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Virell, S., Lander, S., Wyman, D., Ye, W.J., Dirock, S., Lander, S., Wayman, D., Ye, W.J., Dirock, S., Lander, S., Lander, S., Wayman, D., Ye, W.J., Dirock, S., Lander, S., Wayman, D., Ye, W.J., Dirock, S., Lander, S., Lander, S., Wayman, D., Ye, W.J., Dirock, S., Lander, S., Roye, M., X., Wyman, D., Ye, W.J., Dirock, S., Lander, S., Mayman, D., Ye, W.J., Allong, S., Mayman, S., Mayman, D., Ye, W.J., Allong, S., Mayman, 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo
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Conservative:
Mismatches:
Indels:
                                                                                                                                       /note="assembly_fragment:00407"
                             /note="assembly_fragment:01790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                     fragment_chain:1
125938. .156004
73351. .125837
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Best Local Similarity:
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103601 119609: conf. 100 bp 119709: gap of 103709 bp in length 119710 118055: contig of 18346 bp in length 1188156 138155: gap of 100 bp 138156 158360: contig of 20205 bp in length 100 bp 138156 158360: contig of 20205 bp in length
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                                                                                                                                                                                                                                      70946: gap of 100 bp
87757: contig of 16811 bp in length
                                                                                                                                                                                                                                                                                                       857: gap of 100 bp
103500: contig of 15643 bp in length
                                                                                                                                                                                                                                                                                                                                                                    103501 103600: gap of 100 bp
103601 119609: contig of 16009 bp in length
                                            84: gap of 100 bp 48095: contig of 5811 bp in length
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/clone_lib="RPC1-11 Human Male BAC"
1. .1629
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/noter"assembly_fragment"
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20727. 25379
/note-"assembly_fragment"
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/note="assembly_fragment"
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/note: assembly_fragment"
119710. 138055
/note: assembly_fragment"
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158461. .190960
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59654. .70846
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16321. .20626
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42285. .48095
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/chromosome:"11"
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                42184: contig of
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48196. .59553
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158361 158460: gap of
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59553: ~~
                                                                                                                                                                             gap of
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Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S.,
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Galagan, J., Gardyans, S., Glode, S., Goyette, M., Graham, L.,
Grand Pierre, N., Grant, G., Hagos, B., Haeford, A., Horton, L.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehocxky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrin, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
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Stange-Thomann, N., Stojanovic, N., Severy, P., Spencer, B.,
Vasilliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Voung, G., Zainou, J., Zimmer, A. and Zody, M., Trigilio, J.,
Direct Suphission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 12, 2000 this sequence version replaced gi:7523857. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 189160; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
Quality coverage: 4.3 in Q20 bases; sum-of-contigs
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Sequencing vector: M13; M7815; 100% of reads Sequencing vector: M13; M7815; 100% of reads Chem.stry: Dye-terminator B19 Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 178632 bases at least Q40 Consensus quality: 185374 bases at least Q20 Consensus quality: 187834 bases at least Q20
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25380 25479: gap of
25480 32157: conti
32158 32257: gap of
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12245 16220: cont
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25379: conf
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LQDAVDEABHPSRVRDS1LSYSAPVYTDVSGAETAKHHDSELDEADADAQIQKLKFIA
AREAAERELATRYAQLEEKHGETLDMVEELKTEJAKAQALSVESSISRTSTPVIRKR
SSQNVMIIORAHRSTATLSNÍ ABENHIADPDYMANFELNILNAMHELIARSVR QÊLER
DVTNAKKEMETKMIIISGLTRERSSLKAASPMDMAMVSSLREQLERSEKHVQELRESN
                                                                                                                                                                                                               LTATYVEIYNETLRDLLIPEHIPQHERGTYTIREDVKGNIILTGLQOVEVNSVDDLMN
VLAQGSALRQTDATAINARSSRSHAVFSLNLVRKGAKGPTAPTDRRMSMPLEAMSGTE
                                                                                                                                                                                                                                                                                 AMVTTDSKMHFVDLAGSERLKNTGAQGERAKEGISINAGLAALGKVISQLSSRQPGAH
VSYRDSKLTRLLQDSLGGNAITYMIACVTQAEFHLSETLNTVQYAQRARAIQSKPRIQ
QVDEGDKQAIIERLKAEVAFLREQIRSSERGGGDRRSMLLAPGERSERQNEREAELQN
                                                                                                                                                                                                                                                                                                                                                                                    ÓLLDARENYTTLSORHAKLISEMAKARENEFAENOHLEESLGESATERLNRSNSFAÓA
VEOVVLEYEKTIOSLEOSLASTRATLANTEATLLEKETKCAYTET INTOLOARLOKLM
OREASTENYLHDLEAKLDSHTSGEEKNATIITELRKEIARVRENEANAEDYISTLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAEADQDAELMQREIDRLEQVIERQRSLGKLDSLLNELDHIQQDPPTIPENEHTNG
GRHRKMASRDYANHSRSQSHVSHRSQFDEPIRESSEEDIPEEDEDNLDATPTDKANTP
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KELKDKPQVDNRWSLQQVEEERKKRVDAERARQHLEERMQSLASGKKKKKGSLNCGGG
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RASDDDVKTAVRVAVRVRPPLGPDDPGYDLVPQRFQRSMVQVQGETGVAIDSPQGRKL
                                                                                                                                          FVFDRVFGPEVDQEGVWEYLSDCVNAFTQGYNVSLLAYGQSGAGKSYTMGTAGPDVQE
                                                                                                                                                                       DLEAMGVIPRAAIALFEKLDGSSPKSQGAASKRSSMSQLRAPSRVAMLQPSNIDKDWK
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complement(2500. .2595)
/gene="B14D6.010"
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/note="39 bp poly(t) tandem repeat"
complement(8041. .8212)
/gene="B14D6.010"
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/number=
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/number=
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/gene="B14D6.010"
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/gene="B14D6.010"
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/gene="B14D6.010"
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/gene="B14D6.010"
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/gene="B14D6.010"
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/gene="B14D6.010"
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/gene="B14D6.010"
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2152. .2178
/note="27 bp c
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Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:
Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:
G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute
of Blochemistry, Heinrich-Heine-University, D-40225 Duesseldorf,
E-mail: ulrich-schulte@uni-duesseldorf.de
on Jan 25, 2002 this sequence version replaced gi:7899304.
Sequencing was performed by WMC Blotech AG, Ebersberg, Germany,
http://www.mwgdna.com
this contig is an assembly of BAC 1406 from 1 to: 69793, cosmid
23D9 from 69794 to: 109492 rev, library pLORIGYGKN, strain
74-OR-23-1A, BAC 519 from 109493 to: 133555 rev, and BAC 1207 from
133556 to: 199386 BAC clones (strain ORYAA) and cosmid clones are
available at the Fungal Genetic Stock Center, http://www.fgsc.net;
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of linkage groups II
Location/Qualifiers
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AL356173
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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5283. 7427,7508. 7831,8041. 8212))
/gene="B14D6.010"
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5283. .7427,7508. .7831,8041. .8212))
/gene="B14D6.010"
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/organism="Neurospora crassa"
/db_xref="taxon:5141"
/chromosome="6"
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/note="overlap to BAC B23D6"
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1760. .8212
/gene="B14D6.010"
                                    Matches:
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Direct Submission
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Rattus norvegicus clone RP31-108E11 strain Brown Norway, WORKING DRAFT SEQUENCE, 10 ordered pieces.
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Benjamin, B., Blakesley, R.W., Bouffard, G.C., Breen, K., Brinkley, C.,
Benjamin, B., Blakesley, R.W., Bouffard, G.C., Breen, K., Brinkley, C.,
Bencoks, S., Dietrich, N.L., Granite, S., Gun, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Larlc, P.,
Lee-Lin, S.-C., Legaspi, R., Maduro, C.L., Maduro, V.B.,
Margulies, E. H., Masiello, C., Maskeri, B., Mastrian, S.D.,
McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eulelcostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Submitted (03-MAY-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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Submitted (30-NOV-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle. Gaithersburg, MD 20877, USA
3 (bases 1 to 207584)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On May 3, 2002 this sequence version replaced gi:17155044.
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Contact: nisc_zoo@nhgri.nih.gov
                                       Mismatches:
Indels:
                                                                                                                                                                                                                               ------ Project Information
                                                                                                                                                                      US-09-966-880A-8 (1-198) x NCB14D6 (1-199386)
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Center clone name: 108E11
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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/gene="B14D6.030"
/note="contains EST gb:BF072791"
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/product="putative protein"
/protein_id="CAD21210.1"
/protein_id="CAD21210.1"
/brotein_id="CAD21210.1"
/brotein_id="cutill375980"
/translation="markrebels.Didratgsffpd.efabennes.umrlyFrHOFOR
TDMQLRDFSGSAYSHCYEDKIELFLTYAFSSNETTALFRLNGFGRYMFKDMSKCFDE
ISKYTCKYGHPLTLOFYIMIRNYRLRLNGRHLEAAWWAEOMELELACHTDEVNNNIRKI
YTHYSDSWNFRIGHWADNRRSMISVLSSAAALCEAIDELREAMASFWSRLSDEEKS
SEMTAHISQLARGLERERAQLDSIAGFFRQLEQRHALLESSHHIMALEHSQRNSQLM
ATAQMQIDLGTTTTRDAKTMKGLAFMGALELPGTFWSAIFSNPFFEFKIDKLWVYFAA
                                                                                                                                                                                                                                                                                                                                                          /translation="MLSHVPPSAQKNVLDDDLDYDNFDLTADDVRPISTSKTPARKEQ
GLSYVDLTGDSQELKSIQGSARTWTQKKTPELDIDISSDGFLDIDSTRSTIRGERTS
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ISGPNISKAAQPTYHDNDDNDDFFASPPPRFTREQKGKGPASTTPDVINIDDSDDDDP
                                                                                                                                                               /note="similarity to product:unknown, clone pp2464, homo sapiens, TREMBL:AF218002_1" /codon_start=1
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17409. .18161
17488. .18161
/gene="B14D6.030"
                                                                                                                                                                                                                                                             /product="conserved hypothetical protein"
/protein_id="Cab21209.1"
/db_xref="GI:18375979"
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Matches:
                                    13243. .15390
/gene="B14D6.020"
13243. .15390
                                                                                                                                     /qene="B14D6.020"
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/gene="B14D6.030"
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/gene="B14D6.030"
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18162. .18246
/gene="B14D6.030"
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/gene="B14D6.030"
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/gene="B14D6.030"
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/gene="B14D6.030"
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20697. .21695
         /number=6
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Mus musculus.
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                                                                                                                             Best Local Similarity:
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                                                                                                                                                         Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
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TITLE
JOURNAL
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AUTHORS
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                                                                                                                                                                                                                          **NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**Jost the finished sequence as soon as it is available and the accession number will be preserved.

**Jost the finished sequence as soon as it is available and the accession number will be preserved.

**Jost the finished sequence as soon as it is available and the accession number will be preserved.

**Jost the finished sequence as soon as it is available and the accession number will be preserved.

**Jost the finished sequence as soon as it is available and the accession number will be preserved.

**Jost the finished sequence as soon as it is available and the accession number will be g523 contig of 9411 bp in length 54012 54013 app of unknown length 69523 contig of 6872 bp in length 69523 gap of unknown length 13549 135548; gap of unknown length 135549 144220; gap of unknown length 135549 145220; gap of unknown length 135549 145220; gap of unknown length 1575471 15777 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 157547 
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                                                                                       Insert size: 199000; agarose-fp
Insert size: 206684; sum-of-contigs
Quality coverage: 10 48x in Q20 bases; agarose-fp
Quality coverage: 10.09x in Q20 bases; sum-of-contigs
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Consensus quality: 205765 bases at least Q40 Consensus quality: 206455 bases at least Q30 Consensus quality: 206619 bases at least Q20
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199518: contig of 27647 bp in length
199618: gap of unknown length
207584: contig of 7966 bp in length.
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/strain="Brown Norway"
/db_xref="taxon:10116"
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46035 c 45902 g 54686 t
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1915. 28903
// note="assembly_fragment"
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/note="assembly_fragment
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/note="assembly_fragment
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1. .41024
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ALE Oppoblished

Barna, N., Bastlen, C., Lander, E., Allen, N., Anderson, S., Barren, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Campoplano, A., Conke, P., Changol, Y., Colangelo, M., Colangelo, Y., Campoplano, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodges, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Hulme, W., Illev, I., Hangos, B., Heaford, A., Horton, L., Hulme, W., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McCarthy, M., McEwan, P., Macdonald, P., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., Macdonald, P., Marquis, N., Mathews, C., McCarthy, M., McDwa, T., Mlenga, V., Morpheters, R., Landers, T., Lehoczky, J., Leyine, R., Liu, G., Morphy, T., Naylor, J., Mguyen, C., Norbu, C., Norbeeters, R., Malong, V., Roman, J., Mhowa, P., McRewan, P., McCann, K., McDennell, P., O'Gail, D., Ollver, J., Retta, R., Ribeack, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Stange-Thomann, N., Tesfaye, S., Theodore, J., Travers, N., Surnos, R., Stange-Thomann, N., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Voung, G., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zahmek, L., Zimmer, A. and Zody, M.

Submitted (15-APR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 11, 2001 this sequence version replaced gi:13625486.

All repeats were identified using Repeatmasker: html

Conter, Whitehead Institute/ MIT Center for Genome Center, Whitehead Institute/ MIT Center for Genome Center.

Conter, Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC091322 232951 bp DNA linear HTG 11-JUN-2001
Mus musculus clone RP23-60D3, WORKING DRAFT SEQUENCE, 5 unordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 23291)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-60D3
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Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                        Indels:
                                                                                                                                                                                                                                              US-09-966-880A-8 (1-198) x AC103892 (1-207584)
                                                                                                                                                                                                                                                                                                                    42 PheSerLeuAspPheGlyTyrLeuArg 50
                                                                                                                                                                                Gaps:
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AC091322.2 GI:14336533
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TITLE
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
              Insert size: 210000; agarose-fp
Insert size: 232551; sum-of-contigs
Quality coverage: 10.7 in Q20 bases; agarose-fp
Quality coverage: 9.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                          54 153: gap of 100 bp 11. Tengen.
154 2590: contig of 2437 bp in length
2591 2690: contig of 2437 bp in length
11775 109524: contig of 9084 bp in length
11775 11874: gap of 100 bp
11875 100524: contig of 88650 bp in length
100525 100524: gap of 100 bp
100625 232951: contig of 132327 bp in length
100525 232951: contig of 132327 bp in length.
1. 232951

/organism="Mus musculus"
//clone="RP23-6003"
/clone="RP23-6003"
/clone="RP23-6003"
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Consensus quality: 232319 bases at least Q20
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Matches:
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/note="assembly_fragment"
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/note="assembly_fragment
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/note="assembly_fragment
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154. .2590
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AE003632 AE002690
AE003632.2 GI:10728720
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AE003632
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KEYWORDS
SOURCE
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ARSADKDIGSDQEENGGCSPLTTATTASPSRSPEPEEDQPEEQSTSBQSIPEQSTPD
HQLENDIKSEAKSEIEPVEDNNNNNAMTKPSSEEREPNASGSMPSSPVAEASAEAAT
ERTPEKEKEKDVEVDVEKPDEAPSSAVPSTEVTLPGGAGAPVTLEAIONMQMAIAQFA
                                                                                                                                                                                                                                                                                                                                                                        AKT IANGSNGADNEAAMKQLAFLQQTLFNLQQQQLFQTQLIQQLQSQLALNQAKQĒED
TEEDADQEQDQEQETDTYEEEERIADMELRQKAEARWAEAKARQHLINAGVPLRESSG
SPAESLKRRREHDHESQPNRRPSLDNTHKADTAQDALAKLKEMENTPLPFGSDLASSI
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HRCRYGGWRYGSDSALQIIRSHTGERFFKCWYGGSRFTYKGNLKVHPGHAOKFPHV
PMNATPIPEHMDKFPPDLLDQMSPTDSSPNHSPAPPDLGSAPASFPAPFDGLONLYRP
PMNATPIPEHMDKFPPDLLDQMSPTDSSPNHSPAPPDLGSAPASFPARFEGGNEY
PMEILKSLGAAAPHQYFPQELPTDLRKPSPQLDEDEPOVKNEPVEEKDOREEHEGGENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPPVVQPIQPAALMHPQSSPGSQSHLDHLPTPGQLPPREDFFAERFPLNFTTAKMLSP
EHHSPVRSPAGGALPPGVPPPHHHPHHMARSPFFNPIKHEMAALLPRPHSNDNSWEN
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PEQIQAAEIRDPPPSMMPGHFMNPFAAAAFHFGALPGGPGGPPGPNHGAHNGALGSES
SQGDMDDNMDCGEDYDDDVSSEHLSNSNLEQEGDRSRSGDDFKSLLFEQKLRIDATGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VÄTNPVRPRSSASSHGHSVGSTSAPTSPSVHASSQVIKRSSSPARSEASGGALDLTPR
AAPTSSSSSRSPLPKEKPVSPPSLPRSPSGSSHASANILTSPLPPTVGIDCLPPGLQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMNQIAQSVMPAAPFNPLALSGVRGSTTCGICYKTFPCHSALEIHYRSHTKERPFKCS
ICDRGFTTKGNLKQHMLTHKIRDMEQETFRNRAVKYVSLPISPIPSYPFHSYS"
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Trautvetteria carolinensis internal transcribed spacer 1, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIEVSNTCETMKLKELMKNKKISDPNQCVVCDRVLSCKSALQMHYRTHTGERPFKCRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          НЕДООНОНЕМОДОДААУАААААДНННОДМААЕНОНОЕДЕВГЕЛЕВАЕЛОДКАЛАЛАЛА
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                                                                                                                                                                                                                                                    /translation="MKNHLSNVLCAMRSDFKDNHQETINKMIQFGTVKYGIVKQLKDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Nucleotide sequence of the Celera sequence differs from the published sequence for this transcript."
/note="salm gene product; Nucleotide sequence of the Celera sequence differs from the published sequence for
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join(172159. .172172,172243. .172896)
/gene="sala"
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Mismatches:
                                                                                                                       /protein_id="AAF53097.1"
/db_xref="G1.7297849"
/db_xref="FLYBASE:FBan0006464"
/db_xref="FLYBASE:FBgn0004579"
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Trautvetteria carolinensis
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join(<52364. .54959,55677. .55837,57830. .58091,58154. .58386,
58476. .58673,58807. .>59160)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Nucleotide sequence of the Celera sequence differs /note-"Nucleotide sequence for this transcript."
/db_xref-"FLYBASE:FBan0004881"
/db_xref-"FLYBASE:FBan0000287"
join(52364. .54959,55677. .55837,57830. .58091,58154. .58386, /gene-"salr"
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LPFGPLGFMGLHPPPNVCNLCFKMLPSLAALESHLQSEHAKEPATGHAQRPQCSDAGS
PYGAKLTLNPNLFAKKPPSSSSSSGSEKLPESSNPPFPAENPPATPIKEDPDQEQLMV
                                                                                                                                                       NTQNYLHGSSGMGSHQNNASPGDPFASYNQNMMNMYTNFKPSYGHSQVGPASVQMGG
EPGLEMGNRMGHSMPESMGFDGGMGSGMGMSNGLGAGMRVGSMRGGQRLAGGYSSNGL
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GQVQGGQYP TRLPFAPPVAPVGGGOHOQVEBEEIRQETPVPAGELSKPWYKEKE
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DRERDLVEHLHIAKLVRRSSASRESQPAEYSLAQMERIIDKSWEDLIEIDKTSETSKL
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KAHMSIHKIKPPMRSQFKCPVCHQKFSNGIILQQHIRIHTMDDGSGGGGAPAANPGEA
ERLGIEDQNSNKSLGTSDTLDFSTTISDHSGQRSESSQGGBFDEFWTMDSTDDSRDNS
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LEMLQRRTEEVLDSASQSLHAAQMQEEYSEYASKEAQSRGEIFKHRCKYCGKIFGSYS
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from the published sequence for this transcript."
/db_xrefe"FLYBASE:FBan0006464"
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complement(join(<122109. .122243,122367. .126202,
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Randazzo,F., Lamson,G., Scott,E.M., Zhang,G., Kassam,A., Pot,D. and
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Skaryota i Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/gene."IGHV4-34"
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Patent: WO 0214500-A 4630 21-FEB-2002;
CHIRON CORPORATION (US) ; Hyseq Inc. (US)
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   /gene∵"IGHV4-34"
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Xiang,Q.Y., Soltis,D.E. and Soltis,P.S. The eastern Asian and eastern and western North American floristic disjunction: congruent phylogenetic patterns in seven diverse
                                                                                                      2 (bases 1 to 245)
Xiang,O.-Y., Soltis,D.E. and Soltis,P.S.
Direct Submission
Submitted (02-APR-1997) Plant Biology, Ohio State University, 1735
Neil Avenue, Columbus, OH 43210, USA
Location/Qualifiers
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Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 354)
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IgM: IgM heavy chain; immunoglobulin mu heavy chain; variable region.
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                                                         Mol. Phylogenet. Evol. 10 (2), 178-190 (1998)
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A48781
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A58739
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                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 569)

Hunt,S., Pavitt,B., Willey,D., Carter,N. and Ross,M.
Direct Submission

Submitted (02-MAR-2000) E-mail contact; humquery@sanger.ac.uk
Marker strSX1703 (Primer A : CTCCTCAGAMGCATTCCTG; Primer B :
TGGTTTATGCTTTGTTTTCCA; amplimer size : 184 bp) was developed from
a single pass sequencing read from H.sapiens flow-sorted chromosome
X random shear fragment, SCXPCO7h12. Vector : pUC18 Site : Smal
Location/Qualifiers
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Penicillium marneffei
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
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2 (bases 1 to 653)
Danchin, A. and Pascal, G.
Direct Submission
Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yuen, K.Y., Pascal, G., Wong, S., Glaser, P., Woo, P., Kunst, P., Cheung, E., Medigue, C. and Danchin, A. Exploring the Penicillium marneffel genome
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/db_xref="taxon:37727"
/clone="pm363.b"
/ 159 c 140 g 178 t
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/organism="Homo sapiens"
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AL158650.1 GI:7161252
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Alignment Scores:

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PAT 06-MAR-1998
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Browne,M.J., Chapman,C.G., Clinkenbeard, Helen,E. and Robinson,J.H.
CHIMMERIC LEPTIN FUSED TO IMMUNOGLOBULIN DOMAIN AND USE
PATENT: WO 9700319-A 2 03-IAN-1997;
SMITHKLINE BEECHAM PLC (GB)
Other publication AU 6011096 970115.
                                                                                                                                                                                                                                            PAT 07-MAR-1997
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Browne, M.J., Murphy, K.E., Chapman, C.G., Clinkenbeard, H.E., Young, P.R. and Shatzman, A.R.
NOVEL COMPOUNDS

Patent: WO 9604388-A 8 15-FEB-1996;
SMTHKLINE BEECHAM PLC (GB)
Other publication AU 3382595 960304.
Location AU 3382595 960304.
Location AU 3382595 960304.

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Sequence 8 from Patent WO9604388.
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Bukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pleryqota:

Neoptera: Endopterygota: Diptera: Brachycera; Muscomorpha:

Ephydroidea: Drosophilidae: Drosophila.

1 (bases 1 to 1101)

1 (champe,M., Brokstein,P., Hong,L., Agbayani,A., Cailson,J., Champe,M., Chavez,C., Dorsett,V., Dresnek,D., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Krommiller,B., Li,P., Liao,G., Miranda,A., Mungall,C.J., Nunoo,J., Pacleb,J., Paradus,V., Park,S., Patel,S., Phouanenavong,S., Man,K., Yu,C., Lewis,S.E., Rubin,G.M.
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Browne, M.Joseph., Young, P.Ronald., Shatzman, A.Richard.,
Murphy, K.Elizabeth., Chapman, C.Gerald. and
Clinkenbeard, H.Elizabeth.
Therapeutic uses of fusion proteins between mutant 11. 4/11.13
antagonists and immunoglobulins
Patent: US 5783181-A 5 21-JUL-1998;
Location, Vouelifiers
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Sequence 5 from patent US 5783181.
AR018705 1GT:3973819
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Browne, M.J., Murphy, K.E., Chapman, C.G., Clinkenbeard, H.E.,
Young, P.R. and Shatzman, A.R.
NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                         Unclassified.

I (bases 1 to 984)
Browner,M.Joseph., Young,P.Ronald., Shatzman,A.Richard.
Murphy,K.Elizabeth., Chapman,C.Gerald. and
Clinkenbeard,H.Elizabeth.
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SMITHKINE BEECHAM PLC (GB)
Other publication AU 3382595 960304.
Location/Qualifiers
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Sequence 8 from patent US 5783181.
AR018707 GI:3973821
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Sequence 5 from Patent W03604388
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Direct Submission

Submitted (03-APR-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley Nathonal Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection I (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAS, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu.) or send email to
condamifiers
1101
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KTKEWTNLDNITFSFDCKRRSVGFYADMEYNCQIFHMCDEDY"
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1 (bases 1 to 1149)

1 vove, M.J., Murphy, K.E., Chapman, C.G., Clinkenbeard, H.E., Young, P.R. and Shatzman, A.R.
NOVEL COMPOUNDS
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/strain="y: cn bw sp"
/db_xref="taxon:7227"
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Matches:
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SMITHKLINE BEECHAM PLC (GB)
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/db_xref="GI:20151855"
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Sequence 6 from Patent W09604388.
A48779
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/note="Longest ORF"
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PAT 05-DEC-1998
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Browne, M.Joseph., Young, P. Konald., Shatzman, A. Richard.,
Murphy, K. Elizabeth., Chapman, C. Gerald. and
Clinkenbeard, H. Elizabeth.
Therapeutic uses of fusion proteins between mutant IL 4/ILl3
                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1149)

Browne, M. J., Murphy, K. E., Chapman, C.G., Clinkenbeard, H.E., Young, P. R. and Shatzman, A. R.

NOVEL COMPOUNDS

Batcht: WO 9604388-A 9 15-FEB-1996;

SMITHKLINE BECKLAM PLC (GB)
Other publication AU 3382595 960304.
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Sequence 6 from patent US 5783181.
AR018706.1 GI:3973820
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Sequence 9 from Patent WO9604388.
A48782
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unidentified.
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unclassified.
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Best Local Similarity:
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Browner, J., Chapman, C.G., Clinkenbeard, Helen, E. and Robinson, J.H.
CHIMERIC LEPTIN FUSED TO IMMUNGCLOBULIN DOMAIN AND USE
Patent: WO 9700319-A 1 03-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                  Unclassified.

(bases 1 to 1149)

Browne, M.Joseph., Young, P.Ronald., Shatzman, A.Richard.,

Browne, M.Joseph., Chapman, C.Gerald. and

Clinkenbeard, H.Elizabeth.

Therapeutic uses of fusion proteins between mutant IL 4/ILl3

antagonists and immunoglobulins

Patent: US 5783181-A 9 21-UL-1998;
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antagonists and immunoglobulins
Patent: US 5783181-A 6 21-JUL-1998;
Location/Qualifiers
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Sequence 9 from patent US 5783181.
AR018708 1 GI:3973822
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Sequence 1 from Patent W09700319.
A58738
A58738.1 GI:3714280
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                                                                                                                                                                                                               /organism="unknown"
344 c 304 g
                                            /organism="unknown"
344 c 302 g
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Hydrastis canadensis NADH dehydrogenase subunit F (ndhF) qene, partial cds; chloroplast gene for chloroplast product. AF238055.2 G1:10710339
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BROWNE, M.J., Chapman, C.G., Clinkenbeard, Helen, E. and Robinson, J.H.
BROWNE, M.J., Chapman, C.G., Clinkenbeard, Helen, E. and Robinson, J.H.
CHIMERIC LEPTIN FUSED TO IMMUNOGLOBULIN DOMAIN AND USE
Patent: WO 9700319-A 3 03-JAN-1997;
SMITHKLINE BEECHAM PLC (GB)
Other publication AU 6011096 970115.
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Eukaryota: Viridiplantee; Streptophyta; Embryophyta: Trach-ophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Ranunculaceae; Hydrastis.
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Indels:
SMITHKLINE BEECHAM PLC (GB)
Other publication AU 6011096 970115.
Location/Qualifiers
1. .1188
/organism-"unidentified"
/db_xreft-"taxon:32644"
T 282 a 369 c 310 g 227 t
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/db_xref="taxon:32644"
369 c 311 g 226
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Sequence 3 from Patent W09700319.
A58740
A58740.1 GI:3714282
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FSTSMLGLVTSSNXIQIYIFXELVGICSYLLIGXWFTRPVAANACQKAFVTNRVGDFG
                                                                                                                                                                                                                                                                                                   LLIGILGEYWITGSFERNDLFEIFWNLIETNEWNFLFVILCAVLLFAGAVAKSAGFPL
HVWLPDAMEGPTPISALIHAATMVAAGIFLIARLIPLFIVIPYIMNISLIGIITVLL
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GIHSMETIVGYSPDPGSUMVLMGGLTKHVPITKTAFLLGTLSLCGIPPLACFWSKDEI
LNDTWLYSPIFAIIAWATAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-JUN-1998) OIIB/NIDR, NIH, 30 Convent Drive MSC4350, Bethesda, MD 20892, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
1 (bases 1 to 1465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Merkel,T.J., Barros,C. and Stibitz,S.
Characterization of the bygR locus of Bordetella pertussis J. Bacteriol. 180 (7), 1682-1690 (1998)
98196709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF071567 1465 bp DNA linear
Bordetella pertussis BvgR (bvgR) gene, complete cds
AF071567
                                                                                                                                                                                                                                                                                                                                                                                                      12 others
                                                                                                                                                /gene="ndhr"
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/db_xref="taxon:16901"
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Mismatches:
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Merkel,T.J., Barros,C. and Stibitz,S.
Direct Submission
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/protein_id="AAC23902.1"
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    1. 1465
    /organism="Bordetella
    /strain="Tohama I"

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Location/Qualifiers
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/transl_table=11
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                                                                                                             /gene="ndhF"
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Asteridae: euasterids I: Garryales; Aucubaceae; Aucuba.

1 (bases 1 to 1237)
Roels, P. and Smets, E.
Broels, P. and Smets, E.
Briect Submission
Submitted (17-APR-1998) K.U.Leuven, Botanical Institute, Laboratory of Plant Systematics, Kard. Mercierlaan 92, 3001 Heverlee, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NASMLGLVTSSNLIQIYIFWELVGMCSYLLIGFWFTRPITAASSCOKARYTURVGDFGL
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                                                                                                                                                                                                                      Submitted (06-001-2000) Dept. of Botany, University of Washington, Box 355325, Seattle, WA 98195-5325, USA Sequence update by submitter on Oct 6, 2000 this sequence version replaced gi:9623118.

Location/Qualifiers
                                                                                       Graham, S.W., Reeves, P.A., Burns, A. and Olmstead, R.G.
Direct Submission
Submitsted (24-FEB-2000) Dept. of Botany, University of Washington,
Box 355325, Seattle, WA 98195-5325, USA
3 (bases 1 to 1230)
Graham, S.W., Reeves, P.A., Burns, A. and Olmstead, R.G.
Direct Submission
               Graham,S.W., Reeves.P.A., Burns,A. and Olmstead,R.G. Long branches in the seed plants and the root of the angiosperms
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Matches:
Conservative:
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/organelle="plastid:chloroplast"
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        /translation="Mihwidarsspeaslspsrrtlrarlapvegptvaelraalkr
DefiparopyvDaggeslegvattiowahriwGlypehcywallyronlhialaqoll
Ogypolaaawrrgnrhygliopepticlasrsysdovlrnubrglpppattlavsps
LLQspyGgoslhslrruracollvlrvstpdaespphldalegiglalmpelmyalr
QGGRAGEAGIRIAQQASAQRIPVMAAGVVDEAMAQAADLLPCRYLLGDHVAPPMTGOR
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Chloroplast Exacum affine
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bormatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Gentianaceae; Exacum.
1 (bases I to 1865)
Olmstead, R.G., Klm, K.J., Jansen, R.K. and Wagstaff, S.J.
The phylogeny of the Asteridae sensu lato based on chloroplast ndhF
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PVAANACQKAFVTNRVGDFGLLLGILGFYWITGSFEFRDLFEIFNNLIYNNEVNFLFV
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RVIPYIMYLISVIGIITVXLGATLAAQKDIKRGLAYSTMSQLGYMHALGMGSYRNA
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SVHFONYSGKQKIPFYSISLMGKGVSKRISKKFCLGTIESSSKRTYRADBNFONMIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1565)
Olmstead, R.G., Kim, K.-J., Jansen, R.K. and Wagstaff, S.J.
Direct Submission
Submitted (03-MAY-1999) Botany, University of Washington, Campus
Box 355325, Seattle, WA 98195, USA
Location/Qualifiers
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Matches:
Conservative:
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                                                                                                           461 g
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PUBMED
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JOURNAL
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/product."poly-beta-hydroxybutyrate synthaso"
/prodein_id="AAM48100.1"
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LVRVVEGEEF.SRQASDGVGAKNPDPMGVGHAFLETTRHWANDPAKIMKAOMTUNDY
LTMOPTTORFEGODAOPYNDARDRERFKDSAMDENTLEDF! KGSYLLASAWMOSTV
NEVDGLDDHTAKKVBFGFYDAMASNRYWTNEFLETTT FETGENLIVKGLIEHLLK
DLERGKGELRISMTDYDAFOVGKNIAVTFGKVVFOTDLMOLIOYTPTTPEVNKRPLMI
VPWINKYTTILDLRENNSFTRANVOGOUSVEVLXSWWNDERIA.TAGKGEDRIYMEGEVLAA
LDALEKVTGEKDVAALGYCLGGTLLASTLSYWAARKDDRIKAGKGPATALSAGEL
SVFIDEEQLTMIESOMAQOGYLDGSKMATTFNMLRANDLIWSFVVNNYILLGKDPFPED
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DHIAPWKSTYMGAHLFSGPVKFVLAASGHIAGVVNPPAAGKYCYWTNAKLPKASDDWL
ASSOTPGSWWPEWNWYYSTESGKVPARNPEKGGLPVLEDAPGSYAKVRIV"
613 c 32 312 t
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Kadouri, D., Burdman, S., Jurkevitch, E. and Okon, Y.
Tdentification and isolation of Genes involved in
Poly(beta-Hydroxybutyrate) Biosynthesis in Azospirillum brasilense
and Characterization of a phbC Mutant
Appl. Environ. Microbiol. 68 (6), 2943-2949 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
Azospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-FEB-2001) Department of Plant Pathology and Microbiology, The Hebrew University Of Jerusalem, Faculty of Agricultural, Food and Environmental Quality Sciences, Rehovot
                                                                                                                                                                                                                                                                                                                                                                             Azospirillum brasilense strain Sp7 bp DNA linear RCT 06-Ju
Synthase (phbC) gene, complete cds.
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                         Matches:
Conservative:
Mismatches:
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Kadouri, D.E., Jurkevitch, E. and Okon, Y.
Direct Submission
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Matches:
Length:
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                                                                                                                                                                                                                                             /strain="Sp7"
/db_xref="taxon:192"
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Azospirillum brasilense
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Hemigraphis alternata NADH dehydrogenase subunit (ndhF) gene, partial cds; chloroplast gene for chloroplast product. U12660.1 GI:607930
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VGIAVLIYSDNYMAHDQGYLRFFAYMSFFSTSMLGLVTSSNLIQIYIFWELVGMCSYL
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NQVRHEPFYLLCAVLLEMBYNSKAGPPLHAUPDAMBGPTPISALHAATWAGVT
VARLDPLEWYLPYIMDPISLIGIITIFLGATHALAQKDIRRGLAYSTMSQLCYMMLAL
GMGSYRSALFHLITHAYSKALLFLGSGSVIHSMESIYGYSPDKNQNIVLMGGLRKHLB
TIKISFLGTFSLCGVPPLACFWSKDEILNDTWATSPIFAITASITAGLTXFYMFRIY
LLTFGGHLNYHFQNYSANQNIFLYSISLMGRACSKILIASITAGLTAGTXFYMFRIY
CHTEGGHLNYHFQNYSANQNIFLYSISLMGRACSKILINDFRLLESFFKNTP
ORDEKINRGRPFINLSFHNKFTFSYYSESDNTMLFSLLILULFTFSFVGSIGIPFNP
NQGGTDILLSFHNKFTFSYYSESDNTMLFSLLILULFTFSFVGSIGIPFNPF
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HFVDRRIIDGITNLVGLLSXFI"
1 303 c 342 g 756 t 2 others
                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Acanthaceae; Hemigraphis. 1 (bases 1 to 1938)
Scotland, R.W., Sweere, J.A., Reeves, P.A. and Olmstead, R.G.
Higher-level systematics of Acanthaceae determined by chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="151 nucleotides from the PCR primer near the 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (26-JUL-1994) Richard G. Olmstead, E.P.O. Biology, University of Colorado, Boulder, CO 80309, USA
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/protein_id="AAA61724.1"
/db_xref="G1:607931"
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/db_xref="taxon:34269"
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Matches:
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Chloroplast Hemigraphis alternata
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/transl_table = 11
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/gene="ndhF"
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AF257485
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      RESULT 98
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                               HAU12660
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7.

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomicsekhri.oc.jp, Tel:81-438-52-3976, Fax:81-438-52-396)

(E-mail:genomicsekhri.oc.jp, Tel:81-438-52-3976, Fax:81-438-52-396)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center tec.); 5- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation: election for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

RAB; annotation: HRI and RAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligo capping; fis (full insert sequence).
Homo saplens cerebellum cDNA to mRNA, clone_lib:BRACE2
clone:BRACE2006249.
                                                                                                                                                                                                                                                                                                                                                           1886 bp mRNA linear Homo sapiens cDNA FLJ36973 fis, clone BRACE2006249. AK094292. GI:21753322 oligo cappient for the same 

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Mismatches:
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Indels:
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/clone_lib="BRACE2"
/note="cloning vector: pME
1 360 c 335 g 651
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/db_xref="taxon:9606"
/clone="BRACE2006249"
                                                                                                                                                       US-09-966-880A-8 (1-198) x AF353205 (1-1857)
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INSFVKQGPKSILWDKIINGIYDWSYNRAYIDTFYTRSF"
313 c 346 g 770 t 19 others
                                                                                            Eukaryota, Vijdiplanter, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Vijdiplanter; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Gesneriaceae; Goyazia. 1 (bases 1 to 1990)
Smith, J.F.
The phylogenetic relationships of Lembocarpus and Goyazia (Gesneriaceae) based on ndhF sequences Ann. Mo. Bot. Gard. (2000) In press
2 (bases 1 to 1990)
Smith, J.F.
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Chloroplast Eremomastax speciosa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Acanthaceae; Eremomastax.
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Submitted (18-APR-2000) Biology, Boise State University, 1910
University Drive, Boise, ID 83725, USA
Location/Qualifiers
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^Aorgania="Goyazia rupicola"
/Grganeile="plastid:chloroplast"
/db_xref="taxon:125973"
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/product="NADH dehydrogenase"
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/db_xref="G1:8453158"
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                                                                                Chloroplast Goyazia rupicola
AF257485
AF257485.1 GI:8453157
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/noter"70 nucleotides from the PCR primer near the 5' end
were unsequenced"
Scotland, R. W., Sweere, J.A., Reeves, P.A. and Olmstead, R.G. Higher-level systematics of Acanthaceae determined by chloroplast DNA sequences.
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/trans1_table:11
/product."NADH dehydrogenase subunit"
/protein_id."AAA61723.1"
/db_xrefo"G1:607929"
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/organism."Eremomastax speciosa"
/organelle:"plastid:chloroplast"
/db_xref:"taxon:37794"
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Olmstead, R.G.
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Submitted (26-JUL-1994) Richard
University of Colorado, Boulder,
Location/Qualifiers
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